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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
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                                                                                                                                                                                                                                                                                                                                                                                   score g
                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                 No. is the number of results predicted by chance to have greater than or equal to the score of the result being posterived by analysis of the total score distribution.
  444444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A_Geneseq_032802:*

1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*

3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*

4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*

5: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*

6: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*

7: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*

8: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*

9: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*

10: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*

11: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*

12: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*

13: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*

14: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*

15: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*

16: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*

17: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*

18: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*

19: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*

20: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*

21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*

22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*

23: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*

24: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*

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26: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*

27: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
                                                                                                                                                                                                                                                                     Match
Query
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57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FLSELNKELEAE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   September 11, 2002, 08:58:47
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                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                          IJ
                  AAR10889
AAR42385
AAR42380
AAR42378
AAR14482
AAR34545
AAR34545
                                                                                                                                                                            AAB62110
AAE04637
AAE04636
                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Search time 75.59 Seconds
(without alignments)
17.633 Million cell updates/sec
                                                                                 Leukotoxin 352 enc
Recombinant leukot
Recombinant leukot
Recombinant leukot
                                                                                                                                                                                                                                                                     Description
                     LKT352. Pasteurel Leukotoxin 352 pro Recombinant leukot
                                                                                                                                                                               Pasteurella haemol Pasteurella haemol
                                                                                                                                                                                                                              M. bovis Dalton
  haemolytica
                                                                                                                                                                                                                                                                                                                                                                                                        printed
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•	AAB64322	22	28	71.9	4 1	45
Exendin agonist, S	AAB64232	22	28	71.9	41	44
	AAE08486	22	28	71.9	41	43
Exendin agonist pe	AAE08396	22	28	_		42
CId	AAY94155	21	28	<u>:</u>	41	41
Amino acid sequenc	AAY94057	21	28	71.9	41	40
gonist	AAB53000	21	28	1.	41	39
4	AAB52903	21	28	1	41	38
	AAB11234	21	28	71.9	41	37
	AAB11144	21	28	71.9	41	36
agonist	AAY17577	20	28	۲	41	35
	AAY24822	20	28	71.9	41	34
Exendin agonist pe	AAY31518	20	28	71.9	41	33
_	AAB21073	21	1098	75.4	43	32
Chimeric protein #	AAW13866	18	1098	75.4	43	31
Bovine IL-2/LKT ch	AAR52747	15	1098	75.4	43	30
Bovine IL-2 - LKT	AAR22103	13	1098	75.4	43	29
Bovine gamma-IFN/P	AAB21074	21	1069	75.4	43	28
Chimeric protein #	AAW13867	18	1069	75.4	43	27
Bovine IFNgamma/LK	AAR52748	15	1069	75.4	43	26
LKT-GnRH chimeric	AAW79569	19	977	75.4	43	25
-	AAW03942	17	977	75.4	43	24
ropneumoni	AAY51410	21	956	75.4	43	23
ApxIIC protein. A	AAW22156	18	956	75.4	43	22
APPA haemolysin an	AAR12561	12	956		43	21
Pasteurella haemol	AAE04638	22	953	75.4	43	20
PtxA protein of Pa	AAR60072	15	953		43	19
Leukotoxin protein	AAR43865	14	953		43	18
Leukotoxin from P.	AAR15159	12	953		43	17
105kD PTX protein	AAR07167	11	953		43	16
Rotavirus VP4-leuk	AAR34548	14	951	75.4	43	15
Somatostatin-leuko	AAR34546	14	943	75.4	43	14
toxin g	AAR34547	14	936	75.4	4 U	13
Leukotoxin 352 pol	AAW79568	19	926	75.4	43	12

ALIGNMENTS

AAB62110;

AAB62110 standard; Protein;

927

A

ب

29-MAY-2001

(first entry)

Moraxella; antigen; immune response; infection; RTX toxin; vaccine; antibacterial; A subunit. M. bovis Dalton 2d RTX toxin A subunit. WPI; 2001-235092/24. N-PSDB; AAF57290. Farn J, 08-MAR-2001. WO200116172-A1. Novel Moraxella bovis antigen useful in compositions for raising immune response in an animal, has protease, lipase or hemolysin activity . (CSIR) COMMONWEALTH SCI & IND RES (UYME) UNIV MELBOURNE. 31-AUG-1999; 31-AUG-2000; 2000WO-AU01048 Moraxella bovis Strugnell R, 99AU-0002571 Tennent J; ORG

Claim

26;

Fig

5

60pp;

English.

Gaps

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RESULT
AAAD4637
ID AAE0
XX AAEC
XX Leuk
XX Leuk
XX Leuk
XX Leuk
XX Immu
XX A Immu
XX A
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Matches
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                                                                                                                           The present sequence is Pasteurella (Mannheimia) haemolytica modified leukotoxin-50 (lkt50) protein. The modification comprises the removal of amino acids within the hydrophobic transmembrane domain of a full length leukotoxin protein. Modified leukotoxin sequences are used in vaccines to treat or prevent diseases associated with leukotoxin, e.g., respiratory disease, and Mannheimia infection (particularly M. haemolytica infection). In addition, the vaccine
                                                                                                                                                                                                                                                                                                                                                             Claim 4; Fig 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified leukotoxin polypeptide is useful in a vaccine to prevent or treat Mannheimia (Pasteurella) infection (particularly M. haemolytica infection), and disease associated with a leukotoxin, e.g., respirato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to new Moraxella bovis antigens and nucleic acid sequences encoding these antigenic polypeptides. The antigenic polypeptides and polynucleotides are useful for raising an immune response in an animal directed against Moraxella, preferably against M. bovis or M. catarrhalis, and for treating Moraxella infections. The present sequence represents the amino acid sequence of the A subunit of
                                                         ruminant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lo RYC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pasteurella haemolytica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leukotoxin 50; lkt50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pasteurella haemolytica modified leukotoxin 50 (lkt50) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE04637 standard; Protein; 450 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leukotoxin 50; lkt50; respiratory disease; infection; ther immunostimulant; antibacterial; vaccine; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              433 flselnkeleae 444
                                                                          used to prepare a medicament. Furthermore, the plant th modified leukotoxin sequences is fed to an animal s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-408470/43
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12; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNIV GUELPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shewen PE,
                                                         to prevent or treat respiratory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           927 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                       70pp;
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                                                                                                                                                                                                                                                                                                                                                          English
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection; therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strommer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
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                                                                             transformed
such as a
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                                                                                                                                                                                                                                                                                                                                                                                                                                       respiratory
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RESULT
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              Matches
                                           Query Match
Best Local
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                       The present sequence is Pasteurella (Mannheimia) haemolytica modified leukotoxin-66 (lkt66) protein. The modification comprises the removal of amino acids within the hydrophobic transmembrane domain of a full length leukotoxin protein. Modified leukotoxin sequences are used in vaccines to treat or prevent diseases associate with leukotoxin, e.g., respiratory disease, and Mannheimia infection (particularly M. haemolytica infection). In addition, the vaccine is used to prepare a medicament. Furthermore, the plant transformed with modified leukotoxin sequences is fed to an animal such as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified leukotoxin polypeptide is useful in a vaccine to pitreat Mannheimia (Pasteurella) infection (particularly M. hi infection), and disease associated with a leukotoxin, e.g., % \left( \frac{1}{2}\right) =\frac{1}{2}\left( \frac{1}{2}\right) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 2; 70pp; English
                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection),
disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pasteurella haemolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-408470/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lo RYC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200144289-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  animal feed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leukotoxin 66; 1kt66; respiratory disease; infection; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pasteurella haemolytica modified leukotoxin 66 (lkt66) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE04636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYGU-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-2000; 2000WO-CA01498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lmmunostimulant; antibacterial;
          Local Similarity hes 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ட
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD08975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNIV GUELPH OFFICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shewen PE,
                                                                                                                                                                                                                                                    to prevent or treat respiratory diseases.
                                                                                                                                                                                      803
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0172148
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75.0%;
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75.0%;
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                                        Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 23;
1; Mismatches
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       Mismatches
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33;
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                                                                         Length 608;
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       Indels
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haemolytica
, respiratory
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.Gaps
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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pasteurella haemolytica proteins vaccines to protect animals esp. e.g. pneumonia.
                                                                                         Haemophilus somnus; immunogenic; haemolysin; LppB; LppC; thromboembolic meningoencephalitis; septicaemia; arthritis; pneumonia; lktA gene; haemin-binding protein; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pAA352 is derived from pAA114, a clone isolated from a genomic library of P. haemolytica. The protein, designated "new leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin. LKT 352 and pref. antigenic fragments of it, can be used in vaccines to protect cattle from respiratory diseases. They can also be used to produce antibodies for immunoaffinity purificn. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-000097/01.
N-PSDB; AAQ10272.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-APR-1989;
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  WO9321323-A
                                               Pasteurella haemolytica.
                                                                                                                                                                                                Recombinant leukotoxin peptide
                                                                                                                                                                                                                                                     19-APR-1994
                                                                                                                                                                                                                                                                                                                                                      AAR42385 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 further proteins. [Fig. contg. sequence v. poor].
See also AAR10890, AAR10909, AAR10910 and AAQ10783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKT; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leukotoxin 352 encoded by plasmid pAA352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 75.0
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               924 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Babiuk LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        haemolytica Al strain B122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90CA-2014033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.4%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        respiratory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43;
Pred. No.
1; Mismatc
                                                                                                                                                                                                                                                                                                                                                         924
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cattle from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 924;
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RESULT
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04-JUN-1992;
04-JUN-1992;
29-MAR-1993;
29-MAR-1993;
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04-JUN-1992;
29-MAR-1993;
29-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The lppB gene protein was expressed in E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene lktA coded for by plasmid pAA352. The llpB gene fragment was taken from pMS11. LppB can be used in vaccines for preventing or treating H. somnus infections, which cause thromboembolic meningo-encephalitis, septicaemia, arthritis and pneumonia in vertebrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus somnus immunogenic proteins used in vaccines selected from haemin-binding protein, haemolysin, LppB and corresp. DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                        09-APR-1992;
                                                                                                                                        05-APR-1993;
                                                                                                                                                                                                                               W09321323-A
                                                                                                                                                                                                                                                                             Pasteurella
                                                                                                                                                                                                                                                                                                                      Haemophilus somnus; immunogenic; haemolysin; LppB; LppC; thromboembolic meningoencephalitis; septicaemia; arthritis; pneumonia; lktA gene; haemin-binding protein; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR42380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR42380 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 11; 119pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harland RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FLSELNKELEAE 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1993-351733/44.
DB; AAQ51086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || |||||:||
fllnlnkelgae 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 75.0
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Theisen
                                                                                                                                                                                                                                                                             haemolytica
                                                                                                                                                                                                                                                                                                                                                                                                                 leukotoxin peptide (split) from plasmid pGCH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfeiffer CG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92US-0893424.
92US-0893426.
93US-0038287.
93US-0038288.
93US-0038719.
92US-0865050.
92US-0893424.
92US-0893426.
92US-0893426.
93US-0038287.
93US-0038288.
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                                                                                                                                        93WO-CA00135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93WO-CA00135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.48;
75.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pontarollo RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB Pred. No. 52; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            À
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and LppC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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RESULT

ARAF42378

ID ARAF4

XX ARAF4

AC ARAF6

AC ARAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                              04-JUN-1992;
04-JUN-1992;
29-MAR-1993;
29-MAR-1993;
29-MAR-1993;
WPI; 1993-351733/44
                                    Harland RJ, Picir
C, Theisen M;
                                                                                                                       (UYSA-)
                                                                                                                                                                                                                                                                             09-APR-1992;
                                                                                                                                                                                                                                                                                                                           05-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                  28-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                             W09321323-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pneumonia; lktA gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR42378 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The hmb gene encoding the haemin-binding protein was expressed in E coli as a fusion to the Pasteurella haemolytica leukotoxin gene lktA coded for by plasmid pAA352. The hmb gene fragment was taken from pRAP504 and starts at the codon for the 33 rd amino acid residuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thromboembolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR42378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of ORF1. The haemin binding protein can be used in vaccines for preventing or treating H. somnus infections, which cause thromboembolic meningo-encephalitis, septicaemia, arthritis and pneumonia in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus somnus immunogenic proteins used in vaccines selected from haemin-binding protein, haemolysin, LppB an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vertebrates.
See also AAR42370-86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harland RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        corresp. DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLSELNKELEAE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fllnlnkelgae 435
                                                                                                                       UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n 75.4%;
Similarity 75.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ51082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Theisen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              somnus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leukotoxin peptide (split) from plasmid pGCH5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 6;
                                                                                                                     SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfeiffer
                                                                                                                                                          93US-0038288.
93US-0038719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mnus; immunogenic; haemolysin; Lpp
meningoencephalitis; septicaemia;
                                                                                                                                                                                                     92US-0893426.
93US-0038287
                                                                                                                                                                                                                                                   92US-0865050
92US-0893424
                                                                                                                                                                                                                                                                                                                      93WO-CA00135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-0038719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                       cG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haemin-binding protein; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English
                                                                       Pontarollo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pontarollo RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ed. No. 52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     haemolysin; LppB; LppC;
                                                                       RA,
                                                                       Potter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potter AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LppB and LppC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT
AAR14482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
contg. the gene was ligated into the Smal site of pucl3 to form pAA179. From this, two constructs were made in the ptac-based vector, pGH432:lacI digested with Smal. One, pAA342, consisted of the 5' AhaIII fragment from lkth while the other, pAA345, contained the entire MaeI fragment. Clone pAA342 expressed a truncated leukotoxin peptide at high levels while pAA345 expressed full
                                                                                                                                                                 Vaccines for Pasteurella haemolytica infection in cattle -comprise sub-unit antigens from P haemolytica fimbrial protein, plasmin receptor, 50 K outer membrane protein and leukotoxin.
                                                            to the same position on gels. The LKT352 gene was prepd. as follows: lkth, conty the gene was ligated into the SmaI sippAA179. From this, two constructs were made
                                                                                                            LKT352 is 98% homologous with authentic leukotoxin and migrates
                                                                                                                                        Disclosure; Fig 5; 92pp; English.
                                                                                                                                                                                                                           WPI; 1991-324967/44.
                                                                                                                                                                                                                                                        Acres
                                                                                                                                                                                                                                                                                                           05-APR-1990;
                                                                                                                                                                                                                                                                                                                                    17-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                               17-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                        W09115237-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The hmb gene encoding the haemin-binding protein was expressed in E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene lkth coded for by plasmid pAA352. The hmb gene fragment was taken from pRAP501 and starts at the codon for the third amino acid residue of ORF1. The haemin binding protein can be used in vaccines for preventing or treating H. somnus infections, which cause thromboembolic
                                                                                                                                                                                                                                                                               (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                   Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen; leukotoxin; vaccine; lktA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKT352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR14482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR14482 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus somnus immunogenic proteins used in vaccines selected from haemin-binding protein, haemolysin, LppB and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See also AAR42370-86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 5; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vertebrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          meningo-encephalitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ51081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FLSELNKELEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fllnlnkelqae
                                                                                                                                                                                                                                                     SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                    Bariuk LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        924 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   haemolytica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                        90US-0504850
                                                                                                                                                                                                                                                                                                                                   91WO-CA00170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       septicaemia, arthritis and pneumonia in
                                                                                                                                                                                                                                                    Potter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  926 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                    Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                    Lawman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                     an MaeI fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lppc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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RESULT
AAR34545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
         and that had been boosted with a conc. culture supernatant of P. haemolytica to increase anti-leukotoxin antibody levels. Positive colonies were screened for their ability to produce leukotoxin by incubating cell lysates with bovine neutrophils and measuring the release of lactate dehydrogenase from the neutrophils. A 4kb fragment was obtd. Progressively larger clones were isolated by chromosome wakking to isolate full length recombinants of ca. 8kb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length leukotoxin at very low levels. The 3' end of the lktA gene of pAA345 was therefore ligated to StyI/BamHI digested pAA342 to yield pAA352 contg. the LKT352 sequence. The protein expressed from the vector can be used to prepare a subunit vaccine with other P. haemolytica antigens, e.g. fimbrial protein, plasmin receptor or 50K outer membrane protein. The vaccines can be used to protect cattle from respiratory diseases such as pneumonia, esp.
                                                                                                                   Gene libraries of P. haemolytica Al (strain B122) were constructed in lambda gtll and pUCl3. Resulting clones were used to transform E coll and individual colonies were pooled and screened for reaction with serum from a calf which had survived a P. haemolytica infection
                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                           Immunological carrier system with enhanced immunogenicity comprises chimeric protein comprising leuco:toxin peptide homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone
                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-1991;
14-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vector; LKT 352; flanking; recombinant; antigen; somatostatin; gonadotropin releasing hormone; rotavirus viral protein 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leukotoxin 352 produced from pAA352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR34545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR34545 standard; Protein; 926
                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ41317.
                                                                                                                                                                                                                                                                                                                                                                                   (UYSÄ-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9308290-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pasteurella haemolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carrier protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              shipping fever pneumonia.
See also AAR14481, 83,84 and 85.
                                                                                                                                                                                                                                                                                                                                                     Hughes HPA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     424 filninkelgae 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FLSELNKELEAE
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                                                                                                                                                                                                                                                                                                                          1993-152482/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 926 AA;
The clone was subjected to
                                                                                                                                                                                                Fig 3; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                      Potter AA,
                                                                                                                                                                                                                                                                                                                                                                                     SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                91US-0779171.
92US-0960932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              92WO-CA00449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lactation; reproduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75
75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 0%;
                                                                                                                                                                                                                                                                                                                                                      Redmond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
52;
restriction enzyme digestion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                             or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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length of the

lktA gene was ligated into pAA342,

yielding

plasmid pAA352.

leukotoxin

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RESULT
AAR50291
Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
      A vaccine comprising an outer membrane protein (OMP) extract of Haemophilus somnus enriched with iron regulated proteins is new. The vaccine pref. further comprises an immunogenic leukotoxin polypeptide, esp. an immunogenic Pasteurella haemolytica leukotox homologous to LKT352. Example 1.2 describes the prodn. of P. haemolytica recombinant leukotoxin from pAA352. Two expression constructs were made. One, pAA342, contained the 5'-AhAII fragment of the ltkA gene, while the other, pAA345, contained the entire lktA gene. pAA342 expressed a truncated leukotoxin at very low levels, while pAA345 expressed full length leukotoxin at very low levels. Therefore, the 3' end of the like page of the leukotoxin at very low levels. Therefore, the 3' end of the leukotoxin at very low levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              high levels and the other expressing the full length leukotoxin at low levels. The 3' end of the lktA gene from the full length clone was ligated to the truncated gene clone to yield plasmid phA352. The clone was used to produce chimeric proteins by gene fusion with an antigen coding sequence, e.g. the coding sequence of somatostatin, gonadotrophin releasing hormone or rotavirus viral protein 4, i.e. leukotoxin works as a carrier protein to bring about a larger leukotoxin works as a carrier protein to bring about a larger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune response than the antigen alone. Immunisation with the antigens can regulate growth rate, lactation and reproductive efficiency. See also AAR34546-8.
                                                                                                                                                                                                                                                   Haemophilus somnus outer membrane protein extract enriched with iron-regulated proteins, opt. contg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine; outer iron regulated
                                                                                                                                                                                                         Claim 5; Fig
                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                       Harland RJ,
                                                                                                                                                                                                                                                                                                                                                                                      (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA2099707-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR50291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR50291 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to yield two clones, one expressing truncated leukotoxin peptide at high levels and the other expressing the full length leukotoxin at
                                                                                                                                                                                                                                         leuco:toxin antigens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                424 filninkelgae 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                     1994-092909/12.
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                                                                                                                                                                                                                                                                                                         AAQ44760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  926 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     haemolytica Al (strain B122)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukotoxin
                                                                                                                                                                                                       5; 78pp; English
                                                                                                                                                                                                                                                                                                                                                       Potter AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane
protein;
                                                                                                                                                                                                                                                                                                                                                                                                                       92US-0908253
                                                                                                                                                                                                                                                                                                                                                                                                                                                      93CA-2099707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.4%;
75.0%;
                                                                                                                                                                                                                                           for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; OMP; Haemophilus somnus;
leukotoxin; Pasteurella haemolyti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid pAA352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43;
Pred. No.
                                                                                                                                                                                                                                           as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haemolytica;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                           Matches
                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
Ţ
                                                                                                                                                                                                                                                    A truncated leukotoxin (AAW03945), LKT 352, lacks the cytotoxic portion of the native protein from Pasteurella haemolytica. It is the product of plasmid pAA352 which carries a truncated lktA gene (AAT37179). A fusion protein (AAW03942) between LKT352 and a gonadotropin releasing hormone tetramer can be expressed in Escherichia coli. This is useful as a vaccine for fertility control, partic. immunological sterilisation of domestic or
                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 3A-3I; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gonadotropin-releasing hormone multimer fusion proteins - w. Leukotoxin polypeptide for increased immunogenicity, useful antifertility vaccine prodn.
                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                        control, partic. farm animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manns JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P. haemolytica truncated leukotoxin (LKT352).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pasteurella haemolytica Al strain B122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukotoxin.

NB: the protein sequence however this protein is compared to the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-AUG-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9624675-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contraceptive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW03945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW03945 standard; Protein; 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leukotoxin; LKT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || |||||:||
424 fllnlnkelqae 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKT352 or new leukotoxin
                               Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FLSELNKELEAE 12
  FLSELNKELEAE 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1996-384447/38.
DB; AAT37179.
                                                                    Similarity 75.09; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potter AA;
                                                                                                                                                                                         926 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       926 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; immunogen; vac
sterilisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0387156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-CA00049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gonadotropin-releasing hormone; GnRH; immunogen; vaccine; fertility control; terilisation; plasmid pAA352.
                                                                                            75.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e in Fig 5
described
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                                                                    Score 43; DB:
Pred. No. 52;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98% homologous to authentic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprises 926 amino acids, in the text as having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
. 52;
                                                                                                                17;
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                                                                                                                Length 926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 926;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                         is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                 0;
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RESULT 13
AAR34547
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AAW79568
ID AAW7
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                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                  The present sequence represents a recombinantly produced or chemically synthesised leukotoxin 352 (LKT 352)polypeptide, derived from the lktA gene that is present in the plasmid phA352. This gene produces a truncated protein that has an estimated molecular weight of about 99 kDa and lacks the cytotoxic portion of the molecular. Thus this gene has a higher expression level than that of the full-length molecule. This can be used in the construction of a chimeric protein that comprises a leukotoxin polypeptide, several multimers, and a ORTH sequence. The
                                   AAR34547 standard;
                                                                                                                                                                                                                                            leukotoxin polypeptide, several multimers, and a GnRH sequence. The chimeric protein can be used as a vaccine to help reduce the incidence of mammary tumours in a mammalian individual.
                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric protein of leukotoxin and gonadotropin releasing useful for, e.g. preparation of vaccines for reduction of of mammary tumours in mammals
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Figure 3.1-9; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-159540/14.
N-PSDB; AAV61530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Manns JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gonadotropin releasing hormone; GnHR; multimer; vaccine; tumour; Leukotoxin
                                                                                                    424 filnInkelgae 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-FEB-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9806848-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW79568 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leukotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW79568;
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                                                                                                                            1 FLSELNKELEAE 12
                                                                                                                                                       Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine;
                                                                                                                                                                                                                       926 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potter AA;
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0694865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-CA00559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 11..924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sing hormone; GnHR; chimera; leukotoxin polypeptide; tumour; Leukotoxin 352; LKT 352; lkth; plasmid pAA352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 926
                                                                                                                                                                  75.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Recombinant leukotoxin peptide"
                                   936
                                                                                                                                                                  Score 43;
Pred. No.
                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Å
                                                                                                                                                                52;
                                                                                                                                                                              19;
                                                                                                                                                    2
                                                                                                                                                                              Length 926;
                                                                                                                                                                                                                                                                                                                                                                                                                                hormone
incidence
                                                                                                                                                    0;
                                                                                                                                                  Gaps
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0;

23-AUG-1993

(first entry)

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AAR34546
ID AAR3
XX
AC AAR3
XX
DT 23-4
XX
DE Soma
                                                                        RESULT
                                                                                                  В
                                                                                                                 Š
                                                                                                                                                                                Query Match
                                                                                                                                                                                                                releasing hormone (GnRH) gene were constructed on a Pharmacia Gene Assembler using standard phosporamidite chemistry. The oligonucleotides were annealed and ligated into vector pAA352 (contg. the Pateurella heamolytica leuko-toxin gene) which had been digested with BamHI. The ligated DNA was used to transform E. coli strain WH3000. Transformants contg. the oligonucleotide inserts were identified by restiction endonuclease mapping and the recombinant plasmid designated pAA502. The chimeric protein produced from the plasmid works to bring about a larger immune response than the antigen
                                                                                                                                                                                                                                                                                                                                   Immunological carrier system with enhanced immunogenicity comprises chimeric protein comprising leuco:toxin peptide homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone
Somatostatin-leukotoxin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-1991;
14-OCT-1992;
                   23-AUG-1993
                                                       AAR34546 standard;
                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                Oligonucleotides contg. sequences from bovine
                                                                                                                                                                                                                                                                                                                  Example 2; Fig 8; 95pp;
                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ41322
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-152482/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09308290-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vector; LKT 352; flanking; recombinant; antigen; somatos gonadotropin releasing hormone; rotavirus viral protein carrier protein; lactation; reproduction; SRIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GnRH-leukotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                           (UYSA-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                  424 fllnlnkelgae 435
                                                                        14
                                                                                                                                    Local Similarity nes 9; Conserv
                                                                                                                   1 FLSELNKELEAE 12
                                                                                                                                                                                                 i.e. the leukotoxin works as a carrier protein. so AAR34545-8.
                                                                                                                                                                                                                                                                                                                                                                                                           HPA,
                                                                                                                                                                                936 AA;
                                                                                                                                     Conservative
                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           Potter AA,
                                                                                                                                                                                                                                                                                                                                                                                                                            SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-0779171
92US-0960932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92WO-CA00449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "recombinant 927..936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                       Protein;
                                                                                                                                             75.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "GnRH"
                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                           Redmond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prod
                                                       943
                                                                                                                                            Score 43;
Pred. No.
 fusion
                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                           M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukotoxin protein"
                                                                                                                                             52;
                                                                                                                                                      14;
                                                                                                                                     2
                                                                                                                                                                                                                                                                                                gonadotrophin
                                                                                                                                                    Length 936;
                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                       or
                                                                                                                                   0;
                                                                                                                                   Gaps
                                                                                                                                    0;
AAR34548
ID AAR3
XX
AC AAR3
AC AAR3
XX
DT 23-A
DT 23-A
KW Vect
KW Gona
                                                                                                                                                                                                          Q
                                                                                                 RESULT
                                                                                                                            망
                                                                                                                                                              Matches
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                                                                                                  15
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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosporamidite chemistry. The oligonucleotides were annealed and ligated into vector pAA352 (contg. the Pateurella heamolytica leukotoxin gene) which had been digested with BamHI. The ligated DNA was used to transform E. coll strain JM105. Transformants contg. the oligonucleotide inserts were identified by restiction endonuclease mapping and the recombinant plasmid designated pAA496. The chimeric protein produced from the plasmid works to bring about a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunological carrier system with enhanced immunogenicity comprises chimeric protein comprising leuco:toxin peptide homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vector; LKT 352; flanking; recombinant; antigen; somatostatin; gonadotropin releasing hormone; rotavirus viral protein 4; carrier protein; lactation; reproduction; SRIF.
Vector; LKT 352; flanking; recombinant; antigen; somatostatin;
gonadotropin releasing hormone; rotavirus viral protein 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotides contg. sequences from bovine somatostatin (SRIF) gene were constructed on a Pharmacia Gene Assembler using standard
                                                                       Rotavirus
                                                                                                                                                                 AAR34548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               works as a carrier protein.
See also AAR34545-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hughes HPA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                      23-AUG-1993
                                                                                                                                                                                                              AAR34548 standard; Protein; 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Fig 6; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-152482/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYSA-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09308290-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       larger immune response than the antigen alone, i.e. the leukotoxin
                                                                                                                                                                                                                                                                                                                             424 filninkelgae 435
                                                                                                                                                                                                                                                                                                                                                                     1 FLSELNKELEAE 12
                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 75.0
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ41321.
                                                                    VP4-leukotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    943 AA;
                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91US-0779171.
92US-0960932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92WO-CA00449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "recombinant leukotoxin protein"
930..943 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "SRIF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                        75.4%;
                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Redmond
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB Pred. No. 53; 1; Mismatches
                                                                       fusion
                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ę,
                                                                       prod
                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ç
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Search completed: September 11, 2002, 08:58:48 Job time: 192 sec
                                                                                                  QΥ
                                                                          DЪ
                                                                                                                               Query Match 75.4%;
Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                       Oligonucleotides contg. sequences from bovine Rotavirus viral protein 4 (VP-4) gene were constructed on a pharmacia Gene Assembler using standard phosporamidite chemistry. The oligonucleotides were annealed and ligated into vector paa352 (contg. the Pateurella heamolytica leuko-toxin gene) which had been digested with BamHI. The ligated DNA was used to transform E. coli strain MH3000. Transformants contg. the oligonucleotide inserts were identified by restiction endonuclease mapping and the recombinant plasmid designated paa501. The chimeric protein produced from the plasmid works to bring about a larger immune response than the antigen alone, i.e. the leukotoxin works as a carrier protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunological carrier system with enhanced immunogenicity - comprises chimeric protein comprising leuco:toxin peptide or homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-1991;
14-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-152482/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hughes HPA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                        424
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                   See also AAR34545-7
                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Fig 8; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ41322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYSA-) UNIV SASKATCHEWAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carrier protein; lactation; reproduction; SRIF.
                                                                     1 FLSELNKELEAE 12
|| ||||:||
24 fllnlnkelgae 435
                                                                                                                                                                                                      951 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potter AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91US-0779171.
92US-0960932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92WO-CA00449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "recombinant leukotoxin protein"
927..951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Rotavirus VP-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 1..926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Redmond MJ;
                                                                                                                               Score 43; DB Pred. No. 53; 1; Mismatches
                                                                                                                                                           DB 14; Length 951;
                                                                                                                               2
                                                                                                                               Indels
                                                                                                                               0;
                                                                                                                               Gaps
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OM protein - protein search, using sw model
September 11, 2002, 08:56:22; search time 40.83 Seconds (without alignments) 2181.602 Million cell updates/sec
                                                                                                                                                                                                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-884-696-2 4646

Run on:

Title: Perfect score: Sequence: 1 MSNINVIKSNIQAGLNSTKS.....SSNALQPITQPTQGILAPSV 927

Scoring table: Gapop 10.0 , Gapext 0.5 BLOSUM62

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	. 15	14	13	12	11	10	9	8	7	6	5	4	ω	2	ם	No.	Result
304.5	305.5	328.5	332.5	332.5	343	365	383	391	403.5	410	411	416	432.5	134	806	809.5	1733	1752	1767.5	1820	1849	1851.5	1928	1959.5	2209.5	2236	2240.5	2325	Score	
	6.6		7.2	7.2	7.4	7.9	8.2	8.4	8.7	8.8	8.8		9.3	9.3	17.3		37.3	37.7	38.0	39.2		39.9		42.2	47.6	•	48.2	50.0	; -	Query
1072	993	1296	. 1990	1944	4936	697	208	2064	1115	1636	1208	1302	1829	1829	1706	1705	866	866	1022	1055	1023	1024	1049	1052	956	955	956	953	Length	
2	N	N	N	N	N	2	N	2	ν	N	Ν	2	Ν	ນ	_	N	Ν	ν	<u> </u>	ب	1	N	-	ب	دم	<u>س</u>	ب	μ.	DB	
G95851	AE1905	C82521	A96188	AH3098	AH2515	F81856	S34238	G82562	A47058	в82736	C82779	C81182	E81086	S35027	OYBRC	S51672	141078	T00227	I39643	A37205	LEECA	S10056	S51784	B49219	A43834	A35254	в33389	в30169	ID	
ble hemoly	outer membrane sec	hemolysin-type cal	probable phosphoes	rhizobiocin/RTX to	hypothetical prote		leukotoxin A - Pas	bacteriocin XF2407	_	hemolysin-type cal			lated	cytotoxin RTX homo	_	adenylate cyclase	hemolysin - Escher	A to	- 7	leukotoxin A - Act	hemolysin A - Esch	hemolysin A - Esch	toxin III - Actino	toxin III - Actino	toxin II - Actinob	leukotoxin A - Pas	toxin II - Actinob	xin A - P	Description	

QУ рь δÃ

66 AKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLS 125

44	43	42	41	40	39	38	37	36	35	34	ω G	32	31	30
259.5	261.5	262.5	262.5	263.5	266	266.5	267.5	268	269.5	276	280	280	287	287.5
ა. თა	5.6	5.7	5.7	5.7	5.7	5.7	51	5 8	ت ھ	5.9	6.0	6.0	6.2	6.2
219	1839	3262	1741	387	2348	589	387	539	1112	650	900	643	1417	3083
N	2	N	2	2	N	2	2	2	2	N	N	N	N	N
B95953	S77626	AH2137	S74910	E95933	AD1841	AD2263	E95995	G95405	н95964	G87572	AC1852	T03518	AG2137	AH2493
probable secreted	mannuronan C-5-epi	hypothetical prote	hemolysin - Synech	probable calcium-b	hypothetical prote	hypothetical prote	hypothetical calci	hypothetical prote	probable outer mem	calcium-binding pr	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote

Query Match 50.0%; Score 2325; DB 1; Length 953; Best Local Similarity 49.9%; Pred. No. 1.6e-111; Matches 464; Conservative 175; Mismatches 264; Indels 26; Gaps 13;	C;Function: C;Function: A;Description: lyses leukocytes A;Description: lyses leukocytes C;Superfamily: hemolysin A; hemolysin A homology C;Superfamily: hemolysin A; hemolysis; exotoxin; hemolysis; lipoprotein; tandem rep C;Keywords: calculum binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem rep F;238-784/Domain: hemolysin A homology <hlya> F;716-807/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X) F;554/Binding site: palmitate (Lys) (covalent) #status predicted</hlya>	A; MOLECULE LYPE: DAYA A; RESIDUES: 1-74.1/D', 7/43-953 <lor> A; RESIDUES: 1-74.1/D', 7/43-953 <lor> A; Cross-references: EMBL:M20730; NID:g150492; PIDN:AAA25529.1; PID:g150494 C; Comment: This organism causes bovine pneumonic pasteurellosis (shipping fever). C; Genetics: A; Gene: 1 kt A</lor></lor>	A;Residues: 947-953 <str> R;LO, R.Y.C.; Strathdee, C.A.; Shewen, P.E. Infect. Immun. 55, 1987-1996, 1987 A;Title: Nucleotide sequence of the leukotoxin genes of Pasteurella haemolytica Al. A;Reference number: S29515; MUID:87306837 A;Accession: S29516</str>	A; MOLECULE LYPE: DNA A; Residues: 1-953 <hig> A; Residues: 1-953 <hig> R; Strathdee, C.A.; Lo, R; Y.C. J. Bacteriol. 171, 916-928, 1989 A; Title: Cloning, nucleotide sequence, and characterization of genes encoding the seven; Reference number: A32051; MUID:89123172 A; Accession: C32051 A; Status: not compared with conceptual translation A; Molecule type: DNA</hig></hig>	DNA 8, 15-28, 1999 A;Title: DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster. A;Reference number: A30169; MUID:89210283 A;Accession: B30169 A;Status: not compared with conceptual translation A:Molecule type: DNA	RESULT 1 B30169 B30169 leukotoxin A - Pasteurella haemolytica (serotype 1) N;Alternate names: lktA protein C;Species: Pasteurella haemolytica C;Date: 12-Oct-1998 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999 C;Accession: B30169; C32051; S29516 R;Highlander, S,K.; Chidambaram, M.; Engler, M.J.; Weinstock, G.M.	ALIGNMENTS
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toxin II - Actinobacillus pleuropneumoniae N; Alternate names: cytolysin II; RTX-toxin II - C; Species: Actinobacillus pleuropneumoniae C; Date: 09-Mar-1990 #sequence_revision 01-Nov C; Accession: B3389; S18853; B43599 C; Chang, Y.F.; Young, R.; Struck, D.K. DNA 8, 635-647, 1989 A; Title: Cloning and characterization of a head, Accession: B33389 A; Accession: B33389 A; MOlecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  {\tt IYGNDGNDRLFGGKGDDILDGGNGDDFIDGGKGNDLLHGGKGDDIFVHRKGDGNDIITDS}
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                                                 hemolysin
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                                                 gene
                                                 from
                                                 Actinobacillus
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                                                (Haemophi
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A;Cross-references: EMBL:x61111; NID:g38939; PIDN:CAA43423.1; PIR:Smits, M.A.; Briaire, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Infect: Immun. 59, 4497-4504, 1991
A;Title: Cytolysins of Actinobacillus pleuropneumoniae serotype A;Reference number: A43599; MUID:92040145
A;Accession: B43599
                            C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: calcium binding: cytolysis; exotoxin; hemolysis; lipoprotein; tandem
F;243-787/Domain: hemolysin A homology <-HIYA>
F;719-801/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
                                                                                                                                                                     A; Gene: apxIIA; C; Function:
                                                                                                                                                                                                                                                  A;Molecule type: DNA;
A;Residues: 1-27.948-956 <SM2>
A;Cross-references: GB:X61111; NID:g38939
C;Comment: This organism causes porche p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-956 <CHA>
A;Cross·references: GB:M30602; NID:g141823; PIDN:AAA87232.1;
A;Experimental source: serotype 5
R;Smits, M.A.; Briaire, J.; Jansen, R.; Smith, H.E.; Kamp, E.
submitted to the EMBL Data Library, July 1991
A;Description: Cytolysins of Actinobacillus pleuropneumoniae
A;Reference number: S18852
     F;557/Binding
                                                                                                               A; Description: C; Superfamily:
                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-956 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: $18853
site: palmitate (Lys) (covalent) #status
                                                                                                                                        attacks blood cell membranes
                                                                                                                                                                                            appA; clyIIA
                                                                                                                                                                                                                                                  porcine pleuropneumonia
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                                                                                                                                           causes
  predicted
                                                                                                                                           cell lysis
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DЪ Вb В Qy Best Loc Matches Query Match 419 396 359 336 299 276 239 216 179 157 121 97 61 37 Local Similarity μ TIEASLTTISTALGAVSAGVSAAAVGSAVGAPIALLVAGVTGLISGILEASKQAMFESVA NKVHDRIVEWEKKH-NKNYFEQGYDSRHLADLQDNMKFLINLNKELQAERVVAITQQRWD NRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWD TIDASVTTINTALAAISGGVGAASAGSLVGAPVALLVAGVTGLITTILEYSKQAMFEHVA TGAVAALITSSIMLAISPLAFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVG DIISGLLSGASAGLILADKEASTEKKAAAGVEFANQIIGNVTKAVSSYILAQRVASGLSS ETITGLLSGISAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLST ASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNL-NFSKTNLGL KHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAK QGNGVQDLVKAANDLGIEVWREERSNLDIAKTSFDTTQKILGFTDRGIVLFAPQLDNLLK MSKITLSSLKSSLQQGLKNGKNKLNQAGTTLKNGLTQTGHSLQNGAKKLILYIPQGYDSG MSNINV--IKSNIQAGL-----TGPVAALIASTVALAVSPLSFLNVADKFKQADLIKSYSERFQKLGYDGDRLLADFHRETG AGLELTNELVGNIASSVQTVDAFAEQISKLGSHLQNVKGLGGLSNKLQNLPDLGKASLGL KNP--KIGNTLGSASSISQNIGKANTVLGGIQSILGSVLSGVNLNELLQNKDPNQLELAK KGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQ Conservative 48.2%; 188; Score 2240.5; DB 1; Pred. No. 3.4e-107; 8; Mismatches 254; -----NSTKSGLKNLYLAIPKDYDPQ Indels Length 53; Gaps 395 335 298 275 238 120 96 60 36 358 15;

Qy В Qy Qy

δÃ 밁 δÃ 뭥 QΥ 밁 Š Дb QУ Db Qγ

> 478 456

> > NNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISNSNGKKTQAL 515

HFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVA---NQIGDLAAISRRIDKISSGKAYVDAFEEGQHQSYDSSVQLDNKNGIINISNIN-RKIQSV

572

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A: Molecule type: DNA
A: Residues: 723-955 < LA3>
A: Residues: 723-955 < LA3>
A: Cross references: EMBL: Z22887; NID: g311824; PI
A: Cross references: EMBL: Z22887; NID: g311824; PI
A: Experimental source: serotype T10
C: Function:
A: Description: attacks cell membranes and causes
C: Superfamily: hemolysin A; hemolysin A homology
C: Keywords: calcium binding: cytolysis; exotoxin
F: 240-786/Domain: hemolysin A homology <HLYA>
F: 718-809/Region: 9-residue repeats (G-G-X-G-[DN
F: 718-726/Region: repeat
                                                                                                                                                                                                                         A: Molecule type: DNA
A: Residues: 745-955 <LA2>
A: Cross-references: EMBL: Z22884;
A: Experimental source: serotype 1
A: Accession: S34235
                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 950-955 <HIG>
A; Residues: 950-955 <HIG>
A; Cross-references: GB: M24197; GB: M34943; GI
A; Lainson, A.F.; Altchison, K.D.; Donachie, submitted to the EMBL Data Library, June 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:Z26247; NID:g400424; PIDN:CAA81206.1; PI R;Highlander, S.K.; Engler, M.J.; Weinstock, G.M.
J. Bacteriol. 172, 2343-2350, 1990
A;Title: Secretion and expression of the Pasteurella haemolytica A;Reference number: A35254; MUID:90236888.
A;Accession: A35254
A;Status; preliminary
                                                                                                                                                                                                                                                                                                                                 A; Description: DNA sequence of the carboxy terminal end A; Reference number: S34235 A; Accession: S34237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: lktA protein
C;Species: Pasteurella haemolytica
C;Date: 10-Aug-1990 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
C;Accession: S37145; A35254; S34237; S34235
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                                          Keywords: calcium binding; cytolysis; exotoxin; 240-786/Domain: hemolysin A homology <HLYA>
                                                                                  Description: attacks cell membranes and causes; Superfamily: hemolysin A; hemolysin A homology
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F;792-800/Region: repeat
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F;556/Binding site: palm
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F;754-762/Region:
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    ---ITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADE
                                            DIFVHRQGDGNDSITESEGNDKLSFSDSNLKDLTFEKVNHHLVI-TNTKQEKVTIQNWFR
                                                                                  DYYIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWY-
                                                                                                                                                 KGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGN
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                                                                                                                                                                                                                                                                                             KIVATLGDGDDNVFVGSGTTEIDGGEGYDRVHYSR-GNYGALTIDATKETEQGSYTVNRF
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Pred. No. 5.9e-107;
8; Mismatches 271;
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A; Reference number: A43834; MUID:92267623

A; Accession: A43834

A; Accession: A43834

A; Molecule type: DNA

A; Residues: 1-956 <BUR>
A; Experimental source: isolate 3714

A; Note: sequence extracted from NCBI backbone (NCBIN:104212, NCBIP:10421:
C; Comment: This organism causes acute fatal septicemia in young pigs.
C; Function:
A; Description: attacks cell membranes and causes cell lysis
C; Superfamily: hemolysin A; hemolysin A homology
C; Keywords: calclum binding; cytolysis; exotoxin; hemolysis; lipoprotein; P; 243-787/Domain: hemolysin A homology CHLYA;
F; 719-901/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LYTYF]-X)
F; 557/Binding site: palmitate (Lys) (covalent) #status predicted
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Burrows, L.L.; Lo, R.Y.
nfect. Immun. 60, 2166-2173, 1992
h;Title: Molecular characterization of an
formed number: A43834; MUID:92267623
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Best Local Similarity
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                                                                                                                                                                      NRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWD 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | CONTROL | CONT
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Pred. No. 1.3e-105;
Prematches 259;
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A;Description: lyses lung macrophages (C;Superfamily: hemolysin A; hemolysin A homology C;Keywords: calcium binding; cytolysis; exotoxin; lipoprotein; tandem F;254-804/Domain; hemolysin A homology <HLYA>F;736-862/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X) F;571,702/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                   R;Jansen, R.; Briaire, J.; van Geel, A.B.M.; Kamp, Infect. Immun. 62, 4411-4418, 1994
A;Title: Genetic map of the Actinobacillus pleuropu A;Reference number: S48042; MUID:95012630
A;Accession: S48043
                                                                                                                                                                                                                                        A; Experimental source: strain 405, serotype 8
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, C; Comment: This orgnism causes porcine pleuropneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X68815; NID:g38956; PIDN:CAA48711.1; PID:g38958 A;Experimental source: strain 405, serotype A;Note: sequence extracted from NCBI backbone (NCBIN:125168, NCBIP:12517 R;Jansen, R.; Briaire, J.; van Geel, A.B.M.; Kamp, E.M.; Gielkens, A.L.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            toxin III - Actinobacillus pleuropneumoniae N;Alternate names: RTX-toxin III (ApxIIIA) C;Species: Actinobacillus pleuropneumoniae
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B49219
                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Cloning and characterization of the A; Reference number: A49219; MUID:93162836
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C;Accession: B49219; S48043; S29958
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                                                                                                                                                                C; Function:
                                                                                                                                                                                        A; Gene: apxIIIA
                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: X80055; NID: g558150;
                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-1052 < JAN2>
                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; nucleic acid sequence not shown;
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A; Residues: 1-1052 < JAN1>
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Infect. Immun. 61, 947-954, 1993
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M.A

Query Match
Best Local Similarity
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Conservative

42.2%; So 42.7%; Pr tive 166;

Score 1959.5; I Pred. No. 1e-92; 6; Mismatches 2

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                                                                                                QELKKLADENKSQKLSASDIASSLNKLVGSMALFGTA 904
                                                                                                                                                       ---GSINIPRWYITSNLONYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITS
                                                                                                                                                                                                              LNGGAGNDVYIFRKGDGNDTLYD---GTGNDKLAFADANISDIMIERTKEGIIVKRNDHS
                                                                                                                                                                                                                                                                                                                   EEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGD-----
                                                                                                                                                                                                                                                                                                                                                         EQGRYSVTRELSGATKILREVIKNQKSAVGKREETLEYRDYELTQSGNSNLKAHDELHSV
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                                                                                                                            HNNGVLTIKDWF-----KEGNKYNHKIEQIVDKNGRKLTAENLGTYFKNAPKADNLLN
                                                                                                                                                                                     LEGGDGSDFYVYRSTSGNHTIYDQGKSSDLDKLYLSDFSFDRLLVEKVDDNLVLRSNESS
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C;Function: C;Function: C;Function: Q;Function: Q;Func
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C; Species: Actinobacillus pleuropneumoniae
C; Date: 14-Jul-1995 #sequence_revision 15-Nov-1996
C; Accession: S51784
R; Chang, Y.F.; Shi, J.; Ma, D.P.; Shin, S.J.; Lein,
DNA Cell Biol. 12, 351-362, 1993
A; Title: Molecular analysis of the Actinobacillus p
A; Reference number: S51783; MUID:93263992
A; Accession: S51784
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A; Residues: 1-1049 <CHA>
A; Cross references: EMBL:L12145; NID:g349605; PIDN:AAA21924.1; PID:g470685
C; Comment: This orgnism causes porcine pleuropneumonia.
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                                                                                                                                                            SPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDG--EASSKLDFSKVIQR-----
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Pred. No. 4.1e-91;
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c;Superfamily: hemolysin A; hemolysin
C;Keywords: lipoprotein
F;247-792/Domain: hemolysin A homology
F;564,690/Binding site: palmitate (Lys
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A; Residues: 1-1024 <HES>
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A;Reference number: S07209
A;Accession: S10056
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C; Date: 19-Mar-1997
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Pred. No. 3.4e-87;
3; Mismatches 308
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A;Cross references: GB:M10133; GB:M12863; NID:gl46377; PIDN:AAA23975.1; A;Experimental source: strain J96, O4 serotype R;Stanley, P; Packman, L.C.; Koronakis, V.; Hughes, C. Science 266, 1992-1996, 1994
A;Title: Fatty acylation of two internal lysine residues required for the A;Reference number: A55387; MUID:95099325
A;Contents: annotation; lysine palmitoylation A;Note: lysine modification is performed by the hlyC gene product
                                                                                                                                                                                                                        C; Date: 30-
C; Accession
R; Felmlee,
                                                                                                                             A; Molecule type: DNA
A; Residues: 1-1023 <FEL>
                                                                                                                                                             A; Reference number: A; Accession: A24433
                                                                                                                                                                        A;Title: Nucleotide sequence of an Escherichia A;Reference number: A24433; MUID:85234404
                                                                                                                                                                                                        R; Felmlee, T.; Pellett, S.; Welch, J. Bacteriol. 163, 94-105, 1985
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;Date: 30-Sep-1988 #sequence_revision
;Accession: A24433; I41280
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903 953 860 898

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PID:g146379

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R; Haertlein, M.; Schiessl, S.; Wagner, W.;
J. Cell Biol. 22, 87-97, 1983
A; Title: Transport of hemolysin by Escheric
A; Reference number: 141280
A; Reference number: 141280
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1, 'T', 3, 'V', 5, 'T', 7-44 <RES>
A; Cross-references: GB:MZ9173; NID:g146337;
A; Gene: hlyA
C; Genettcs:
A; Gene: hlyA
C; Function: attacks blood cell membranes
C; Superfamily: hemolysin A; hemolysin A hom
C; Keywords: calcium binding; cytolysis; exception: 9-residue repeats (G-G-X:F;563,689/Binding site: palmitate (Lys) (cc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563,689/Binding site: palmitate (Lys) (covalent) #status experimental
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  VEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLF-
                                                                           EAGSYTVNRKVARGD--IYHEVVKRQETKVGKRTETIQYRDYELRKV-GYGYQSTDNLKS
                                                                                                                 VGNNQYREIRIESHLGDGDDKVFLSAGSANIYAGKGHDVVYYDKTDTGY--LTIDGTKAT
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                                        EAGNYTVTR-VLGGDVKVLQEVVKEQEVSVGKRTEKTQYRSYEFTHINGKNLTETDNLYS
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-	¥.	Db	: : :: : : 718 VBELIGTTRADKFFGSKFADIFHGADGDDHIEGNDGNDRLYGDKGNDTLSGGNGDDQLYG 777
		Qy	729
		Db	778 GDGNDKLIGGAGNNYLNGGDGDDELQVQGNSLAKNVLSGGKGNDKLYGSEGADLLDGGEG 837
D		Qy	751 DDVLNGGAGNDVYIFRKGDGNDTLYDGTG-NDKLAFADANISDIMIERTKEGIIVKRND- 808
٥		Db	838 NDLLKGGYGNDIYRYLSGYGHHIIDDDGGKDDKLSLADIDFRDVAFRREGNDLIMYKAEG 897
		Qy	809HSGSINIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKK 860
	tandom repeat.	Db	898 NVLSIGHKNGITFKNWFEKESGDISNHQIEQIFDKDGRVITPDSLKKALEYQQSN 952
;	n, candem repeat,	Qy	861DGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMALFGT 903
		Db	953 NKASYYYGNDALAYGSQGNLNPLINEISKIISAAGNFDVKEERAAASLLQLSGNASDFSY 1012
		Qy	904 A-NSVSSNA 911
g	25:	Db	1013 GRNSITLTA 1021
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C;Species: Actinobacillus actinomycetemcomitans
C;Date: 16-Sep-1992 #sequence_revision 01-Nov-1996 #text_change 31-Mar-2000
C;Accession: A37205; A60768; B34345; A32276; PH0267; PH0266; S17284 R;Kraig, E; Dailey, T; North 1990 R:Kolodrubetz, D.; Dailey, T.; Ebersole, Infect. Immun. 57, 1465-1469, 1989 C; Accession: sing nucleotide A;Cross-references: GB:X16829; NID:g38643; PIDN:CAA34731.1; PID:g38645 A;Note: the authors present evidence that the nucleotide sequence is co A; Molecule type: DNA A; Residues: 1-1055 <KRA> A; Accession: A37205 A; Title: Nucleotide sequence of the leukotoxin A; Reference number: A37205; MUID: 90202154 leukotoxin A - Actinobacillus actinomycetemcomitans T.; Kolodrubetz, D. J.; Kraig, gene Ħ from sequence is correct Actinobacillus actinomyceten 'n

A; Accession: A; Title: Cloning and expression of the leukotoxin gene A; Reference number: A60768; MUID:89212893 A; Status: nucleic acid sequence not shown; not compared with A60768 from Actinobacillus conceptual translation actinomyce

the

A;Note: this sequence is revised in reference A37205
R;Lally, E.T.; Golub, E.E.; Kieba, I.R.; Talchman, N.S.; Rosenbloom, J.;
J. Biol. Chem. 264, 15451-15456, 199
A;Title: Analysis of the Actinobacillus actinomycetemcomitans leukotoxin
A;Reference number: A34345; MUID:89359382
A;Accession: B34345 A; Molecule type: DNA A; Residues: 297-309,'Y',311-364;434-440,'KC',443-474,'H',476-489,'S',491-493,'VLK',4! Rosenbloom,

gene. Deline

A; Molecule type: DNA
A; Residues: 1-239, 'Y', 241-259, 'H', 261-335, 'A', 337-415, 'S', 417-438, 'S', 440-723, 'N', 72!
PVKRYPLRHCRPITTLTUTQIR' <LALL>
A; Cross-references: GB: M27933
A; Cross-references: GB: M27933

R;Lally, E.T.; Kieba, I.R.; Demuth, D.R.; Rosenbloom, J.; Blochem. Blophys. Res. Commun. 159, 256-262, 1989 A;Title: Identification and expression of the Actinobacill A;Reference number: A32276; MUID:89165863 A;Accession: A32276 the Actinobacillus

actinomycetemcomitans

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A; Note: this sequence is revised in refe R; Ohta, H.: Miyagi, A.; Kato, K.; Fukui, submitted to JIPID, July 1995 A; Description: Modulation of leukotoxin A;Molecule type: DNA
A;Residues: 430-438,'S',440-476,'R',478-506,'RVRS',511,'QSIAINSLNTD',523-541,'I',543
A;Note: this sequence is revised in reference A34345
DONATA H: Mivagi, A.; Kato, K.; Fukui, K. A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A; Reference number: PH0266 A; Accession: PH0267 leukotoxin production γd growth rate and bicarbonate 'n

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A; Molecule type: protein
A; Residues: 2-6, 'L', 8-26 <
C; Genetics:
A; Gene: ltxA
C; Function:
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A;Experimental source: strain
A;Accession: PH0266
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Best Local Similarity
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                           {\tt FNDVFHGHDGDDLIYGYDGDDRLYGDNGNDEIHGGQGNDKLYGGAGNDRLFGEYGNNYLD}
                                                                                                                    YHEVYKRQETKYGKRTETIQYRDYEL--RKYGYGYQSTDNLKSYEEYIGSQFNDVFKGSK
                                                                                                                                                      GAKDDYVFVGSGSTIVNAGDGYDVVDYSK-GRTGALTIDGRNATKAGQYKVERDLSGTQV
                                                                                                                                                                             KAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDI
                                                               FNDIFHSGEGDDL-
                                                                                           LQETVSKQETKRGKVTDLLEYRNYKLDYYYTNKGFKAHDELNSVEEIIGSTLRDKFYGSK
                                                                                                                                                                                                                 RKTRQSGKYEFITELKVKGRTDWKVKGVPNSNGVYDFSNLIQHAVTRDNKVLEARLIANL
                                                                                                                                                                                                                                              RERLTNGKYSYINKLKFGRVKNWQVTDGEASSKL-DFSKVIQR-VAETEGTDEIGLIVNA
                                                                                                                                                                                                                                                                                                            SGKAYADAFEDGKKVEAGSN----ITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTES 528
                                                                                                                                                                                                                                                                                                                                          NYFENGYDARHSAFLEDSLKLFNELREKYKTENILSITQQGWDQRIGELAGITRNGDRIQ 496
                                                                                                                                                                                                                                                                                                                                                              NYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIK 472
                                                                                                                                                                                                                                                                                                                                                                                                      AGVGAASAGSLVGAPIGLLVSAITSLISGILDASKQAVFEHIANQLADKIKAWENKY-GK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNVLSTLSSFLGTALAGIELDSLIK---KGDAAPDA-LAKASIDLINEIIGNLSQSTQTI 176
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GGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDG
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1.4e-85;
nes 298;
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A;Description: attacks blood cell membranes and causes cell lysi C;Superfamily: hemolysin A; hemolysin A homology C;Keywords: calcium binding; cytolysis; extoxin; hemolysis; lip: F;243-789/Domain: hemolysin A homology cHIVA>
F;721-847/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LYIYF]-X) F;560,686/Binding site: palmitate (Lys) (covalent) #status predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Actinobacillus pleuropneumoniae
C;Date: 19-Uul-1996 #sequence_revision 08-Nov-1996 #text_change 18-Jun-1999
C;Accession: 139643; S18769; T39645; S60732; S35781
R,Jansen, R.; Briaire, J.; Kamp, E.M.; Gielkens, A.L.; Smits, M.A.
Infect. Immun. 61, 3688-3695, 1993
A;Title: Structural analysis of the Actinobacillus pleuropneumoniae-RTX-toxin I (ApxI A;Reference number: 139641; MUID:93366425
                                                                                                                                                                   C; Function:
                                                                                                                                                                                            A;Gene: apxIA
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                                                                                                                                                                                                                                               C; Comment: This
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                                                                                                                                                                                                                                                                                              A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                 A;Title: The RTX haemolysins ApxI and ApxII are major virulence A;Reference number: S60731; MUID:95131743
A;Accession: S60732
                                                                                                                                                                                                                                                                                                                                                                                                                        A; MoLecule type: DNA
A; Rosidues: 1-209, 'AMPYLTLA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022 <RE2>
A; Residues: 1-209, 'AMPYLTLA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022 <RE2>
A; Cross-references: EMBL: X68595; NID: 9505568; PIDN: CAA48586.1; PID: 9505570
R; Tascon, R.I.; Vazquez-Boland, J.A.; Gutierrez-Martin, C.B.; Rodriguez-Barbosa, Mol. Microbiol. 14, 207-216, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Sequence analysis and transcription of the apxI operon (hemolysin A;Reference number: I39644; MUID:94237497
A;Accession: I39645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-209, 'AMPYLTLA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022
A; Cross-references: EMBL: X52899; NID: g38949; PIDN: CAA37081.1; PID: g38950
R; Frey, J.; Haldimann, A.; Nicolet, J.; Boffini, A.; Prentki, P.
Gene 142, 97-102, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Nucleotide sequence of the hemolysin A;Reference number: S18769; MUID:91348845 A;Accession: S18769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross references: EMBL:X73117; NID:g312897; A;Frey, J.; Meier, R.; Gygi, D.; Nicolet, J. Infect. Immun. 59, 3026-3032, 1991
                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; not
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A; Residues: 1-1022 < RES>
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                                                                                              YGRHIIIEKGGDDDTLLLSDLSFKDVGFIRIGDDLLVNKRIGGTLYYHEDYNGNALTIKD
                                                                                                                                                            RFTDIFHGAKGDDEIYGNDGHDILYGDDGNDVIHGGDGNDHLVGGNGNDRLIGGKGNNFL
                                                                                                                                                                                                                                              VLKEVVKTQDISVGKRSEKLEYRDYELSPFELGNGIRAKDELHSVEEIIGSNRKDKFFGS
                                                                                                                                                                                                                                                             IYHEVVKRQETKVGKRTETIQYRDYELR--KVGYGYQSTDNLKSVEEVIGSQFNDVFKGS
                                                                                                                                                                                                                                                                                             EKNDRIYLSSGSSIVYAGNGHDVAYYDKTDTGY--LTFDGQSAQKAGEYIVTKELKADVK
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                                                                                                                                                                                                                                                                                                                                                                                              KAYADAFEDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VDAFAEQLGKLGNALSNTR-LSGLASKLNNLPDLSLAGPGFDAVSGILSVVSASFILSNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSAAKSGAGALKNGLGQVKQAGQKLILYIPKDYQASTGSSLNDLVKAAEALGIEVHRSEK
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YN---ALPQLRKDIEQIISSTGAFTGDHGKVSVGSGGPL
                                                                     WYITSNLONYOSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADEN
                                                                                                                                               NGGDGDDELQVFEGQYNVLLGGAGNDILYGSDGTNLFDGGVGNDKIYGGLGKDIYRYSKE
                                                                                                                                                                                                                                                                                                                                               RKQTGKYEYMTELFVKGKEKWVVTGVQSHNAIYDYTNLIQLAIDKKG-EKRQVTIESHLG
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                                                                                                                      ---KLAFADANI---
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A;Gene: hlyA
A;Gene: plasmid pO157
A;Genome: plasmid pO157
C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: cytolysis; hemolysis; lipoprotein; toxin
F;233-776/Domain: hemolysin A homology <HLYA>
F;550,675/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AB011549; NID:g4589740; PIDN:BAA31774.1; PID:g3337015
A;Experimental source: strain EHEC 0157:H7, substrain RIMD 0509952
A;Burland, V.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R R;Burland; P.S. Sofia, Blattner, F.R Nucleic Acids Res. 26, 4196-4204, 1998
A;Title: The complete DNA sequence and analysis of the large virulence plasmid A;Reference number: 222068; MUID:98391744
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A;Experimental source: strain EDL933; serotype O157:H7
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A; Residues: 1-998 <BUR>
A; Cross-references: EMB
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A; Reference number: Z14127; N
A; Accession: T00227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSNIQAGLNSTKSGLKNLYLAIPKDYDPOKGGTLNDFIKAADELGIARLAEEPNHTETAK 67
                  RYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAF
                                                                                     SAVGAPIALLVAGVTGLISGILEASKQAMFESVANRLOGKILEWEKQNGGQNYFDKGYDS 421
                                                                                                                                                                                                             AAAGIELTTQVLGNVGKAVSQYILAQRMAQGLSTTAASAGLITSAVMLAISPLSFLAAAD
                                                                                                                                                                                                                                                                                    LNQLGSFLSSKPRLSSVGGKLQNLPDLGPLGDGLDVVSGILSAVSASFILGNSDAHTGTK
                                                                                                                                                                                                                                                                                                      LAKLGSTISQAKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKK 241
                                                                                                                                                                                                                                                                                                                                                         LONFTGIALSGMALDELLRKOREGEDISONDIAKSSIELINOLVDTVSSINSTVDSFSEO
                                                                                                                                                                                                                                                                                                                                                                          LSSFLGTALAGIELDSLIKK----GDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                              KSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGL-DSVENIDRKLGKASNVLST 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHAAFLEDSLSLLADFSRQHAVERAVAITQQHWDEKIGELAGITRNADRSQSGKAYINYL 493
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Infect. Immun. 63, 1055-1061, 1995

N.Title: Molecular analysis of the plasmid-encoded hemolysin of Reference number: I41077; MUID:95172699

A.Accession: I41078

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Molecule type: DNA

A.Residues: 1-998 <RESS

A.Cross-references: EMBL:X79839; NID:g860924; PIDN:CAA56234.1; PC:Superfamily: hemolysin A; hemolysin A homology

C:Superfamily: hemolysin A; hemolysin A homology

F:233-776/Domain: hemolysin A homology <HLYA>

F:550,675/Binding site: palmitate (Lys) (covalent) #status predi
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C;Species: Escherichia coli
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jul-2000
C;Accession: I41078
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Infect. Immun. 63, 1055-1061, 1995
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                               LSSFLGTALAGIELDSLIKK----GDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQ
                                                               QFFGAAEKVVGLTERGVAIFAPQLDKLLQKY--QKVGSKIGGTAENVGNNLGKAGTVLSA
                                                                                 KSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGL-DSVENIDRKLGKASNVLST
                                                                                                                            KSAFNTASSSVRSAGKKLILLIPDNYEAQ-GVGINELVKAADELGIEIHRTERDDTAIAN
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                                                                                                                                                                                            Similarity 39.9
90; Conservative
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Pred. No. 3.8e-81;
74; Mismatches 312
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A; Molecule type: DNA
A; Residues: 1-1705 <BET>
A; Cross-references: EMBL: Z37112
                                                                    submitted to the EMBL Data Library, September 1994 A; Description: The adenylate cyclase-hemolysin gene A; Reference number: $51672
                                                                                                                       adenylate cyclase hemolysin - Bordetella bronchiseptica C;Specias: Bordetella bronchiseptica C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change C;Accession: S51672 R;Betsou, F.; Sismeiro, O.; Danchin, A.; Guiso, N.
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                                                            A; Reference number: A; Accession: S51672
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calmodulin-sensitive adenylate cyclase catalytic domain homo:

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C;Superfamily: cyclolysin, camera.
C:Keywords: tandem repeat
F;15-328/Domain: calmodulin-sensitive adenylate cyclase catalytic domain homology
F;543-1084/Domain: hemolysin A homology <HLYA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQRALQGAQAVAAAQRLVHAIALMTQFGRAGSTNTPQEAASLSAAVFGLGEASSAVAETV
                                                                                                                                                     WGHDGNDTIHGRRGDDILRGGLGLDTLYGEDGNDIFLQDDETVSDDIDGGAGLDTVDYAA 1213
                                                                                                                                                                                                                                                                                                          AGDDRLDGGAGNDTLVGGEGHNTVVGGAGDDVFLQDLGVWSNQLDGGAGVDTVKYNVHQP 109:
                                                                                                                                                                                                                                                                                                                                                                                     TQKTAYGKRTENVQYRHVELARVGQ-LVEVDTLEHVQHIIGGAGNDSITGNAHDNFLAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLANASRIHYDGGAGTNTVSYAALGRQDSITV----SADGERFNVRKQLNNANVYREGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVK 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSEFTTFVETVGKQDRWRTRDGAADTTIDLAKVVSQLVDANGVLKHSIKLEVIGGDGDDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYADAFEDGKKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGFFRGSSRWAGGFGVAG------GAMALGGGIGAVGAGMSLTD-DAPAGQKA 564
                                                                          MI----HAGNIVAPHEYGFGIEADLSEGWVRKAARRGMDYYDSVRSVENVIGTSMKD-VL 1268
                                                                                                                                                                                         NGGAGNDVYIFRKGD-----GNDTLYDGTGNDKLAFADANISDIM-----IERTKEGI 802
                                                                                                                                                                                                                                 SEERLERMGDTGIHADLQKGTVEKWPALNLFSVDHVKNIENLHGSSLNDSIAGDDRDNEL
IGDAQANTLMGQGGDDTV 1286
                                    ITSDQIDKILQDKKDGTV
                                                                                                              IVKRNDHSGSINIPRWY - - - ITSNLQNYQSNKTDHK - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----QAKGFSNIGNKLQNLNFSKTNLGLEIITGLLSGISAGFALADKNASTGKKV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.48;
                                      864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 809.5; D
Pred. No. 1.9e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333;
                                                                                                                                                                                                                                                                                                                                                    -LDGGSG---
                                                                                                              ---IEQLIG---KDGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                        -----DDVL 754
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A;Title: Secretion of cyclolysin, the calmodulin-sensitive adenylate cyclase-haemol. A;Reference number: S02386; MUID:89091151
A;Contents: annotation; identification of adenylate cyclase-hemolysin bifunctional | R;Munier, H.; Gilles, A.M.; Glaser, P.; Krin, E.; Danchin, A.; Sarfati, R.; Barzu, O Eur. J. Biochem. 196, 469-474, 1991
A;Title: Isolation and characterization of catalytic and calmodulin-binding domains A; Reference number: S14100; MUID:91177021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Superfamily: cyclolysin; calmodulin-sensitive adenylate cyclase catalytic domain he (Keywords: calcium binding; calmodulin binding; cAMP biosynthesis; carbon-oxygen ly: F:15-328/Domain: calmodulin-sensitive adenylate cyclase catalytic domain homology <AU F:25-35/Region: calmodulin binding #status predicted F:59-66/Region: nucleotide binding #status predicted F:544-1085/Domain: hemolysin A homology <HLVA>
F:1033-1041.1042-1050.1174-1182,1289-1297,1298-1308,1316-1324,1430-1438,1556-1564/Ref:983/Binding site: palmitate (Lys) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Species: Bordetella pertussis
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C:Accession: S00993; S:14100; S02389
R:Glaser, P.; Ladant, D.; Sezer, O.; Pichot, F.; Ullmann, A.; Danchin, A.
Mol. Microbiol. 2, 19-30, 1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Contents: annotation; lysine palmitoylation C;Comment: B. pertussis, the etiological agent of whooping cough, disrupts mammalian ation by host cell calmodulin of the adenylate cyclase activity of bacterial cycloly. C;Comment: Adenylate cyclase activity is activated upon binding of calmodulin in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Hackett, M.; Guo, L.; Shabanowitz, J.; Hunt, D.F.; Science 266, 433-435, 1994
A;Title: Internal lysine palmitoylation in adenylate A;Reference number: A55167; MUID:95025937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-78,'M',80,'M',82-97,'M',99-139,'M',141-178,'M',180-399
A;Residues: 1-78,'M',80,'M',82-97,'M',99-139,'M',141-178,'M',180-399
R:Hackett, M.; Guo, L.; Shabanowitz, J.; Hunt, D.F.; Hewlett, E.L.
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A; Residues: 1-1706 <GLA>
A; Cross-references: EMBL: Y00545; NID: g396665; PIDN: CAA68613.1;
R; Glaser, P.; Sakamoto, H.; Bellalou, J.; Ullmann, A.; Danchin,
EMBO J. 7, 3997-4004, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: The calmodulin-sensitive adenylate cyclase of A;Reference number: S00893; MUID:88216178 A;Accession: S00893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cyclolysin - Bordetella pertussis
N;Alternate names: adenylate cyclase precursor; calmodulin-sensitive adenylate cycla:
N;Contains: adenylate cyclase (EC 4.6.1.1), calmodulin-sensitive; hemolysin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
   637
                                                                                                                                                                                                                                                                                                                                                                                                             459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 GLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLI-----KKGDAAP------ 151
                                                                   310
                                                                                                                                                                                                                                                                                                                                          194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYDSLDGV----GSRSFSLGEVSDMAAVEAAELEMTRQVLHAGARQDDAEPGVSGASAHW 458
   DKLAQESSAYGYEGDALLAQLYRDKTAAEGAVAGVSAVLSTVGAAVSIAAAASVVGAPVA
                                                               DEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAVGAPIA 369
                                                                                                                                   GGTVELASSIALALAAARGVTSGLQVAGASAGAAAGALAAALSPMEIYGLVQQSHYADQL
                                                                                                                                                                                            GNVTKAISSYVL----AQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANAL
                                                                                                                                                                                                                                                                                                                                          KGFSNIGNKLQNLNFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQVI
                                                                                                                                                                                                                                                                                                                                                                                                             GQRALQGAQAVAAAQRLVHAIALMTQFGRAGSTNTPQEAASLSAAVFGLGEASSAVAETV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----DALAKA----SIDLINEI----IGNLSQSTQTIEAFSSQLAKLGSTISQ-A 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247;
                                                                                                                                                                                                                                                                      SGFFR-GSSRWAGGFGVAGGAMALGGGIAAAVGAGMSLTD-DAPAGQKAAAGAEIALQLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.3%; Score 806; DB 1; 27.2%; Pred. No. 2.8e-33; tive 142; Mismatches 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1706;
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, A. .
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RESULT 15
S35027
Cytotoxin RTX homolog frpC - Neisseria meningitidis
Cyspecies: Neisseria meningitidis
A;Thompson, S.A.; Wang, L.L.; Sparling, P.F.
Mol. Microbiol. 9, 85-96, 1993
A;Title: Cloning and nucleotide sequence of frpC, a second gene from Neisseria meningitidis
A;Accession: S35026; MUID:94018616
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                                                                                                                Query Match
Best Local Similarity
Watches 237; Conserva
                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-1829 <THO>
A;Cross-references: GB:L06299; NID:g293961; PIDN:AAA99902.1; PID:g293963
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A;Gene: frpC
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                                                      478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           812 SINIPRWY---ITSNLQNYQSNKTD------HKIEQLIG---KDGSYITSDQIDKI 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  813 V-AGQPVVLDVAAGGIDIASRKGER-PALTFITPLAAPGEEQRRRTKTGKSEFTTFVEIV 870
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  95 LQKHSTNKLAK-GLDSVE----NIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGD- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  724 DDRLFGGKG-----
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                                                                           43 DFIKAAD----ELGIARLAEEPNHTETAKKSVDTVNQFL----SLTQTGIAISATKLEKF 94
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                                           DNTKLADGSFAKHGYAALAELDSNGDNIINAADAAFQTLRVWQDLNQDGIS------ 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGGDD---ILRGGLGLDTLYGEDGNDIFLQDDETVSDDIDGGAGLDTVDYSAMI----HPG
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                                                                                                                                  9.3%; Score 434; DB 2; Length 1829; ilarity 22.4%; Pred. No. 3.7e-14; Conservative 159; Mismatches 355; Indels 306;
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866 TSQELKKLADENKSQKLSASDIASSLNKLVGSMALFG 902 : : : : 1402SDRLYAYQSGSTLNGGLGDDYLYG 1425	Фр
1352 AKDDSGQVTVQSYFQNDGSGAYRIDEIHFDNGKVLDVATVKELVQQSTDG 1401	Db 43
DVLNGGAGNUVILEKKGUGNDELTDGTG-NDKLAFADANISDHMIERTREGIIVK 80	5 g 5
1 KGSK#ND1FHSGBGDDLLDGGAGDDRLFGKGNDRLSGDEGDDLLDGGSGD 7	Db 04
YRDYELRKV	Db Qy
635 YTVNRKVARGDIY	Фр
608 HDRVFYSKDGGFGNITVDGTSATEAGS	Qy Db
572 AB-TEGTDEIGLIVNAKAGNDDIFVGQGKMNIDGGDG 607 : : :	ОУ
522 LTAGTESRERLTNGKYSY-INKLKFGRVKNWQVTDGEASSKLDFSKVIQRV 571	Оу
466 KLGERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISN-SNGKKTQALHFTSPL 521	Оу
424 AAYLANNIKFLSELNKELEAERVIAITQQRWDNNIGELAG	Оy
365 GAPIALLVAGVTGLISGILEASKQAMFESVANRL-QGKILEWEKQNGGQNYFDKGYDSRY 423 776 NDTFTLDFSGLVQAFNHVKETNPQKAFVDLAEMLAYGELRSWYEGRRLMADYVEEAKK 833	Qy Db
305 HANALDEFAKOFRKFGYDGDHLLAEYQRGYGTIEASLTTISTALGAVSAGVSAAAVGSAV 364 :	Оy
246 FELSNOVIGNVTKAISSYVLAQ-RVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKEN 304	Qу
187 GSTISO-AKGFSNIGNKLQNLNFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAÅG 245 : : :	Qу
587 LHSRFKDKVELTAEQAKAANLAGIGRLRDLREAAALSGDLANMLKAYSAAETKEAQLALL 646	Db 43
YKDVNKNIGN-GNTLAQQGSYTKTDGTTAKMGDLLLAADN	Db Db

Search completed: September 11, 2002, 09:00:12 Job time: 230 sec

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Maximum DB seq
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Copyright (c) 1993 - 2000 Comp
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ApxIIIB protein.
A. pleuropneumoni
                                                                                                                                                                                                                                                                                       Description
                                                                                                                   Leukotoxin AppIIIA
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AAU34347	AAP70435	AAU37416	AAW27248	AAW07637	AAY51410	AAW22156	AAR12561	AAB21073	AAW13866	AAR52747	AAR22103	AAB21074	AAW13867	AAR52748	AAR76991	AAY51406	AAW22152	AAW79569	AAW03942	AAE04638	AAR60072	AAR43865	AAR15159	AAR07167	AAR34548	AAR34546	AAR34547	AAW79568	AAW03945	AAR50291	AAR34545	AAR14482	AAR42378
Staphylococcus aur		Staphylococcus aur	Pseudomonas fluore	P. suis leukotoxin	A. pleuropneumonia	ApxIIC protein. A	APPA haemolysin an	Bovine IL-2/Pasteu	Chimeric protein #	Bovine IL-2/LKT ch	Bovine IL-2 - LKT	Bovine gamma-IFN/P	Chimeric protein #	Bovine IFNgamma/LK	LhaA (low homology	A. pleuropneumonia	ApxIA protein. Ac	LKT-GnRH chimeric	LKT-GnRH protein f	a haemo	PtxA protein of Pa	Leukotoxin protein	Leukotoxin from P.	105kD PTX protein	Rotavirus VP4-leuk		==		P. haemolytica tru	Recombinant leukot	Leukotoxin 352 pro		Recombinant leukot

ALIGNMENTS

29-MAY-2001 AAB62110;

(first entry)

AAB62110 standard; Protein;

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Moraxella; antigen; immune response; infection; RTX toxin; vaccine; antibacterial; A subunit. M. bovis Dalton 2d RTX toxin A subunit. Novel Moraxella bovis antigen useful in compositions for raising immune response in an animal, has protease, lipase or hemolysin activity Farn (CSIR) COMMONWEALTH SCI & IND RES (UYME) UNIV MELBOURNE. 31-AUG-1999; 31-AUG-2000; 2000WO-AU01048 08-MAR-2001. WO200116172-A1 Moraxella bovis. 2001-235092/24 DB; AAF57290. J, Strugnell R, 99AU-0002571. Tennent J; ORG

leukot

Claim

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Fig

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Best Local :
                                                 preparations are bacterial preparations comprising one or more isolated and purified strains of a microorganism that produces one or more RTX toxins, where the strains have at least one cell-associated RTX toxin. The preparations are used for production of vaccines for the prophylaxis and treatment of infectious diseases caused by microorganisms that produce RTX toxins, where the strains have been attenuated or
                                                                                                                                  AAW22151-W22161 represent A. pleuropneumoniae RTX (repeat in toxins) toxins. These sequence are encoded by the apxICA, apxIBD, apxIIAB°C, apxIIIABCD genes (see AAT73217-T73220), and can be expressed by microorganisms used in the presentations of the invention. The
      pleuropneumoniae infection (swine pleuropneumonia). It h that A. pleuropneumonia produces significant quantities
                                   inactivated. The vaccines are preferably against Actinobacil
                                                                                                                                                                                                                    Disclosure; Pages 107-110; 151pp; English.
                                                                                                                                                                                                                                                  pleuro-pneumonia
                                                                                                                                                                                                                                                                  Preparations - especially
                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTX toxin; apxICA gene; apxIBD gene; apxIIAB/C gene; apxIIIABCD gene; repeat in toxins toxin; cell-associated RTX toxin; vaccine production; therapy; A. pleuropneumoniae infection; swine pleuropneumonia.
                                                                                                                                                                                                                                                                                                                                                        MacInnes J,
                                                                                                                                                                                                                                                                                                                                                                                     (UYGU-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to new Moraxella bovis antigens and nucleic acid sequences encoding these antigenic polypeptides. The antigenic polypeptides and polynucleotides are useful for raising an immune response in an animal directed against Moraxella, preferably against M. bovis or M. catarrhalis, and for treating Moraxella infections. The present sequence represents the amino acid sequence of the A subunit of the RTX toxin from M. bovis Dalton 2d.
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Pred. No.
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                       It has been found
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cell-associated

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Best Local
                                                     This invention describes a novel bacterial preparation (I) which comprises one or more isolated and purified strain(s) of a microorganism, cultured in tryptone yeast extract (TYE) broth, which produces one or more RTX toxins (belonging to the family of toxins referred to as Repeats in Toxins), where the strain(s) have at least one RTX toxin which is cell-associated. The products of the invention have immunostimulatory, antimicrobial, antiinflammatory, antiarthritic and antiabortive activity. The bacterial preparation may be used as vaccines for the prophylaxis and treatment of infectious diseases caused by strains of microorganisms which produce one or more RTX toxins. The infectious diseases are symmetric controlled to the controlled to the controlled to the controlled toxing the 
                  pleuropneumonia, pneumonia, septicemia, nephritis and arthritis septicemia, nephritis, endocarditis and arthritis in piglets; s)
                                                                                                                                                                                                                                                                                                                                                                            Bacterial preparation comprising microorganisms which produce a fof the Repeats in Toxins (RTX) family, useful for treating swine pleuropneumonia, arthritis in swine, shipping fever and abortion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiinflammatory; antiarthritic; antiabortive; trepleuropneumonia; septicemia; nephritis; arthritis; shipping fever; abortion; whooping cough; sleepy for
                                                                                                                                                                                                                                                                                                                    Disclosure; Column 77-84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mallard B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAZ88587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6019984-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTX toxin; vaccine; Repeats in Toxins; immunostimulatory; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A. pleuropneumoniae apxIIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                that the whole-cell protein composition of the cultures corresponds the whole-cell protein profiles obtained from cells recovered at necropsy from the pleural fluid of infected swine. Vaccination with bacterin prepared from heat-inactivated cultures having significant quantities of cell-associated RTX toxins give significant protection swine against challenge with homologous strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYGU-) UNIV GUELPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              passive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY51412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY51412 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FNDIFHSGEGDDLL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             frdifhgadgddll 760
                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunization;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1049
                                                                                                                                                                                                                                                                                                                                                              sleepy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosendal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9505-0396244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0772270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                foal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peritonitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s
  cattle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75
71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apxIIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MacInnes
                                                                                                                                                                                                                                                                                                               96pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
whooping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        meningitis; gastroenteritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ricciatti P;
  cough,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB .
ว. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sleepy foal disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1049;
                  in piglets; shipping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                       in swine
                                                                                                                                                                                                                                                                                                                                                                                                                             member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               joint ill;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR54781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                joint ill (purulent nephritis, arthritis) in foals; septicemia, polyarthritis and abortion in horses; and uninary infections, peritonitis, meningitis, and gastroenteritis. The bacterial preparations may also be used to prepare antibodies which may be used as a means of passive immunization. This sequence represents the Actinobacillus passive immunization approach in the method of the
                                                                                                                                                                                                                      05-NOV-1992;
03-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                          Key
                               The AppIIIA gene having the sequence given in AAQ64827 was isolated from phage lambda clones yfc 26–28 and yfc 31–32 of a genomic library of A. pleuropneumoniae ser. 2. The gene encodes a novel
                                                                           Disclosure; Fig 3; 65pp;
                                                                                                 and as diagnostic reagents
                                                                                                         DNA encoding Actinobacillus pleuropneumoniae leukotoxin - used prepare prods. for use in vaccines for porcine pleuropneumonia
                                                                                                                                         N-PSDB; AAQ64827.
                                                                                                                                                      WPI; 1994-167130/20
                                                                                                                                                                            Chang Y;
                                                                                                                                                                                                                                                        04-NOV-1993;
                                                                                                                                                                                                                                                                             11-MAY-1994
                                                                                                                                                                                                                                                                                                   W09409821-A
                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                              Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                    Leukotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leukotoxin AppIIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR54781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR54781 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
                                                                                                                                                                                                (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 747 frdifhgadgddll 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FNDIFHSGEGDDLL 14
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                    A. pleuropneumoniae ser.
(sequence AAR54781).
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1244
                                                                                                                                                                                                                                                                                                                                                                                                                                   AppIIIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                      92US-0972229.
93US-0072285.
                                                                                                                                                                                                                                                        93WO-US10500
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AA,
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
327 345
                                                                                                                                                                                                                                                                                                                                              'label- transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                   abel=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   pleuropneumonia; vaccine; diagnostic.
                                                                                                                                                                                                                                                                                                                                     587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 48;
                                                                                                                                                                                                                                                                                                                        transmembrane
                                                                                                                                                                                                                                                                                                                                                                  transmembrane
                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 58; E
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                        domain
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Query Match

75.3%;

Score

58;

DB 15;

Length 1244;

13-MAR-1996

(first entry)

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RESULT
AAR76990
ID AAR7
XX
AC AAR7
XX
DT 13-M
                                                                                                                                                                                                        RESULT
AAR86998
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                                                                                                                        Ωy
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                                                                                                                                                          Query Match
Best Local
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                                                                                                                                                Matches
                                                                                                                                                                                                                                                            Enterohaemorrhagic E.coli (EHEC) associated with enterohaemorrhagic colitis, haemolytic uremic syndrome and mesenteric adenitis have been found to carry a hlyA gene and a hylB gene, separated by an intergenic region. The hly genes and the intergenic region are absent from bacteria not associated with these diseases and so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterohaemorrhagic Escherichia coli; virulent; EHEC; O157:H7 serotype; detection; probe; primer; hlyA gene; enterohaemorrhagic colitis; haemolytic uremic syndrome; mesenteric adenitis.
                                                                                                                                                                                                                            provide a useful target for detecting EHEC pathogens, serotype E.coli. The present sequence is that of the encoded by the EHEC hlyA gene.
                                                                                                                                                                                                                                                                                                                                                         EHEC
                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                Claim 1; Columns 37-42; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hall RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5475098-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli (enterohaemorrhagic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterohaemorrhagic E.coli hlyA gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR86998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR86998 standard; Protein;
                       AAR76990;
                                           AAR76990 standard;
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                 Entero:haemorrhagic E. coli (EHEC) nucleic acid sequences for probe and primer design for sensitive and specific detec
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                   480 fndifhgadgndyi 493
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                                                                                                                           1 FNDIFHSGEGDDLL
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                                                                                                                                                Similarity
8; Conserv
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                                                                                                                                                Conservative
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                                                                                                                                                                                                        ΑA;
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                                           protein;
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                                                                                                                                                           67.5%;
57.1%;
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                                                                                                                                                          Score 52; DB Pred. No. 1.4;
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                                                                                                                                                Mismatches
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                                                                                                                                                                      17;
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                                                                                                                                                                    Length
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protein
                                                                                                                                                                                                                                                                                                                                                                   detection
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RESULT
AAE04637
ID AAE0
XX AAE0
AC AAEC
XX Past
DT 10-s
XX Leu)
KW Leu)
KW Leu)
KW immu
KW anir
XX Past
OS Synt
XX
PN WO2
XX
PD 21-
XX
XX 15-
PR 15-
XX 17-
                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                             Matches
17-DEC-1999;
                                        21-JUN-2001
                                                            WO200144289-A2
                                                                                Synthetic
                                                                                                                 animal
                                                                                                                                                                                                                                                                                                                                                                                      AAR76990 represents a repeat region of the lhaA (low homology to appA) gene product which is a toxin component. The repeat region and full gene product are useful as the active ingredient in vaccines for the prophylaxis of Actinobacillus (Haemophilus) pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Region
                    15-DEC-2000; 2000WO-CA01498
                                                                                          Pasteurella
                                                                                                                                                       Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A vaccine contg. a product of the LhaA gene as the active ingredient - for prophylaxis of Actinobacillus (Haemophilus) pleuropneumoniae infectious diseases.
                                                                                                                                   Leukotoxin 50; lkt50;
                                                                                                                                                                            10-SEP-2001
                                                                                                                                                                                                AAE04637;
                                                                                                                                                                                                                   AAE04637 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NISK ) NIPPON SEIBUTSU KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP07138185-A
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                                                                                                                         lmmunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                 infectious (Ap1) diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ap1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinobacillus
                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                       1 FNDIFHSGEGDD
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                                                                                                                                                                                                                                                                   ftdifhgakgdd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat;
                                                                                                             feed;
                                                                                                                                                                                                                                                                                                            Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 8; 15pp;
                                                                                                                                                                                                                                                                                                                                                              127
                                                                                                                                                     haemolytica modified
                                                                                          haemolytica
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                              mutant;
                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine;
 99US-0172148
                                                                                                                                                                                                                                                                                                                                                              AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93JP-0152264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93JP-0152264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pleuropneumoniae
                                                                                                                       antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= repeat_region
/note= "tandem repeat units
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                     26
                                                                                                                                                                                                                                                                                                                    63.6%;
66.7%;
                                                                                                              mutein
                                                                                                                                respiratory disease; infection; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxin repeat (RTX) region
                                                                                                                                                                                                                   450
                                                                                                                                                                                                                                                                                                           Score 49; DB
Pred. No. 0.62
1; Mismatches
                                                                                                                                                                                                                                                                                                            ₩
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KENKYUSHO
                                                                                                                       vaccine;
                                                                                                                                                                                                                   A
                                                                                                                                                    leukotoxin 50 (lkt50) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunisation; pneumonia;
                                                                                                                                                                                                                                                                                                               DB .
1.62;
                                                                                                                      transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZH
                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                             Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acids"
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                          0;
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RESULT
AAE04636
            Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
Modified leukotoxin polypeptide is useful in a vaccine to prevent or treat Mannheimia (Pasteurella) infection (particularly M. haemolytica infection), and disease associated with a leukotoxin, e.g., respiratory
                                                                                                                                                                                                                                                                     17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pasteurella haemolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             animal feed; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pasteurella haemolytica modified leukotoxin 66 (lkt66) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences are used in vaccines to treat or prevent diseases with leukotoxin, e.g., respiratory disease, and Mannheimia i (particularly M. haemolytica infection). In addition, the value of the control o
                                                                                                                                                                            Lo RYC,
                                                                                                                                                                                                                      (UYGU-) UNIV GUELPH
                                                                                                                                                                                                                                                                                                                 15-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                  21-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                               WO200144289-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leukotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE04636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE04636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is Pasteurella (Mannheimia) haemolytica modified leukotoxin-50 (lkt50) protein. The modification comprished removal of amino acids within the hydrophobic transmembrane the removal of aful length leukotoxin protein. Modified leukotoxin domain of a full length leukotoxin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified leukotoxin polypeptide is useful in a vaccine to prevent or treat Mannheimla (Pasteurella) infection (particularly M. haemolytica infection), and disease associated with a leukotoxin, e.g., respiratory disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is used to prepare a medicament. Furthermore, the plant transformed with modified leukotoxin sequences is fed to an animal such as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lo RYC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mmunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ruminant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYGU-) UNIV GUELPH OFFICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    α
                                                                                                                           2001-408470/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ndllhggkgddi 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDIFHSGEGDDL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-408470/43.
                                                                                                       AAD08975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 58.7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD08976.
                                                                                                                                                                       Shewen PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; Protein; 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shewen PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to prevent or treat respiratory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66; lkt66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450 AA;
                                                                                                                                                                                                                                                                                                                   2000WO-CA01498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; 70pp; English.
                                                                                                                                                                                                                                                                  99US-0172148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibacterial; v
                                                                                                                                                                                                                        OFFICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.6%;
58.3%;
                                                                                                                                                                         Lee RWH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RWH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49;
Pred. No.
                                                                                                                                                                     Hodgins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hodgins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease;
                                                                                                                                                                     Ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transgenic
                                                                                                                                                                       Strommer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strommer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Claim 2; Fig disease

2

70pp;

English.

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RESULT
AAR10889
ID AAR10889
ID AAR10889
ID AAR1
AC AAR1
AC AAR1
AC AAR1
AC LEUK
XX LKT;
XX PAST
XX O6-A
XX O6-A
XX O7-C
PF 07-L
PX ACCC
XX PPI
ACCC
XX PPI
ACCC
XX PPI
CC LEUI
CC LEUI
CC See
XX Seq
SQ Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                           Plasmid pAA352 is derived from pAA114, a clone isolated from a genomic library of P. haemolytica. The protein, designated "new leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin. LKT 352 and pref. antigenic fragments of it, can be used in vaccines to protect cattle from respiratory diseases. They can also be used to produce antibodies for immunoaffinity purificn. of further proteins. [Fig. contg. sequence v. poor].

See also AAR10890, AAR10909, AAR10910 and AAQ10783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is Pasteurella (Mannheimia) haemolytica modified leukotoxin-66 (lkt66) protein. The modification comprises the removal of amino acids within the hydrophobic transmembrane domain of a full length leukotoxin protein. Modified leukotoxin sequences are used in vaccines to treat or prevent diseases associated with leukotoxin, e.g., respiratory disease, and Mannheimia infection (particularly M. haemolytica infection). In addition, the vaccine is used to prepare a medicament. Furthermore, the plant transformed with modified leukotoxin sequences is fed to an animal such as a ruminant, to prevent or treat respiratory diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                CA2014033-A
                                                                                                                                                               Claim 13;
                                                                                                                                                                                                          Pasteurella haemolytica proteins and genes - vaccines to protect animals esp. cattle from
                                                                                                                                                                                                                                                                                                Acres
                                                                                                                                                                                                                                                                                                                                                           07-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                       06-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                    07-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKT; vaccine; antigen; respiratory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR10889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR10889 standard;
                                                                                                                                                                                                                                                                                                                            (UYSA-) UNIV SASKATCHEWAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leukotoxin 352 encoded by plasmid pAA352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      429 ndllhggkgddi 440
                                                                                                                                                                                            ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 NDIFHSGEGDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                            pneumonia.
                                                                                                                                                                                                                                                                   1991-000097/01.
                                                                                                                                                                                                                                                                                                SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
7; Conserv
                                                                                                                                                                                                                                                       AAQ10272
                                                                                                                                                               Fig
                                                                                                                                                                                                                                                                                                Babiuk LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       809
   924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haemolytica Al strain B122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                             5; 87pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ā
                                                                                                                                                                                                                                                                                                                                                           89US-0335018.
                                                                                                                                                                                                                                                                                                                                                                                       90CA-2014033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.6%;
58.3%;
                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                Potter AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                Lawman MJP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         shipping fever pneumonia.
                                                                                                                                                                                                        used for producing respiratory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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747 ndllhggkgddi 758

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NDIFHSGEGDDL 13

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RESULT 1
Query Match
Best Local Similarity
7; Conserv
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Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-1992;
04-JUN-1992;
04-JUN-1992;
04-JUN-1993;
29-MAR-1993;
29-MAR-1993;
29-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                   Harland R. Rioux C,
                                                                                                                                  The lppB gene protein was expressed in E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene lkth coded for by plasmid pAA352. The llpB gene fragment was taken from pMS11. LppB can be used in vaccines for preventing or treating H. somnus infections, which cause thromboembolic meningo-encephalitis, septicaemia, arthritis
                                                                                                                                                                                                                       Disclosure; Fig 11; 119pp; English.
                                                                                                                                                                                                                                                   and corresp. DNA
                                                                                                                                                                                                                                                               Haemophilus somnus immunogenic proteins used in vaccines selected from haemin-binding protein, haemolysin, LppB an
                                                                                                                                                                                                                                                                                                                        WPI; 1993-351733/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus somnus; immunogenic; haemolysin; Lpp thromboembolic meningoencephalitis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR42385;
                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                            (UYSA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-OCT-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09321323-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR42385 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  745 ndllhggkgddi 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NDIFHSGEGDDL
                                                                                                            pneumonia in vertebrates. also AAR42370-86.
                                                                                                                                                                                                                                                                                                                                                                RJ,
                                                                                                                                                                                                                                                                                                                                                                                             VINU
                                                                                                                                                                                                                                                                                                           AAQ51086.
                                                                                                                                                                                                                                                                                                                                                   , Pfeiffer
Theisen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lktA
                                                                                924 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haemolytica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukotoxin peptide
             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                             SASKATCHEWAN
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                                                                                                                                                                                                                                                                                                                                                                                                                        92US-0865050.

92US-0893424.

92US-0893426.

92US-0893426.

93US-0038288.

93US-0038288.

93US-0038719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93WO-CA00135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene; haemin-binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
                          63.6%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.6%;
58.3%;
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9
                                                                                                                                                                                                                                                                                                                                                                 Pontarollo
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Pred. No.
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                          Score 49; I
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             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid
                                                                                                                                                                                                                                                                                                                                                                 RA,
                       DВ
1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
5.7;
                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                   Potter AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pCRR28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LppB; LppC;
mia; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ņ
             2
                                       Length 924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 924;
                                                                                                                                                                                                                                                                 LppB and LppC
             Indels
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             Gaps
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RESULT 12
AAR42378
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AAR42380
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XXXXXX
                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-1992;
04-JUN-1992;
04-JUN-1992;
29-MAR-1993;
29-MAR-1993;
29-MAR-1993;
                                                                                                                                                                                                                                                                        The hmb gene encoding the haemin-binding protein was expressed in E. coll as a fusion to the Pasteurella haemolytica leukotoxin gene lktA coded for by plasmid pAA352. The hmb gene fragment was taken from pRAP504 and starts at the codon for the 33 rd amino acid residue of ORF1. The haemin binding protein can be used in vaccines for preventing or treating H. somnus infections, which cause thromboembolic
         19-APR-1994
                                AAR42378;
                                                     AAR42378
                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 6; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus somnus immunogenic proteins used in vaccines selected from haemin-binding protein, haemolysin, LppB and selected from haemin-binding protein, haemolysin, LppB and selected from haemin-binding protein, haemolysin, LppB and selected from haemin-binding proteins used in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus somnus; immunogenic; haemolysin; LppB; LppC; thromboembolic meningoencephalitis; septicaemia; arthritis; pneumonia; lktA gene; haemin-binding protein; fusion protein.
                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ51082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09321323-A
                                                                                                                                                                                                                                          See also
                                                                                                                                                                                                                                                     vertebrates
                                                                                                                                                                                                                                                               meningo-encephalitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harland RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYSA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR42380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR42380 standard; Protein;
                                                                                                               747
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rioux C,
                                                                                                                        2 NDIFHSGEGDDL 13
                                                                                                                                                                                                                                                                                                                                                                               corresp. DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                      1993-351733/44.
                                                                                                              ndllhggkgddi 758
                                                                                                                                                           Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VINU
                                                     standard; Protein;
                                                                                                                                                                                                                                         AAR42370-86.
                                                                                                                                                                                                                   924
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Theisen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leukotoxin
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haemolytica.
        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfeiffer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93US-0038287.
93US-0038288.
93US-0038719.
                                                                                                                                                                                                                   ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92US-0893424.
92US-0893426.
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                                                                                                                                                                      63.6%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cc,
                                                                                                                                                                                                                                                               septicaemia, arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pontarollo RA,
                                                                                                                                                          Score 49; DB
Pred. No. 5.7;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           924
                                                     924
                                                                                                                                                           ω
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                                                     A
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                                                                                                                                                                      DB 14;
5.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potter AA;
                                                                                                                                                                                                                                                               and pneumonia
                                                                                                                                                          2:
                                                                                                                                                                                Length 924;
                                                                                                                                                                                                                                                                                                                                                                                        LppB and LppC,
                                                                                                                                                          Indels
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RESULT :
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Best Local
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04-JUN-1992;
04-JUN-1992;
                                                                                                                                                                                                                                                                                                                                 The hmb gene encoding the haemin-binding protein was expressed in E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene lkth coded for by plasmid pAAS52. The hmb gene fragment was taken from pRAP501 and starts at the codon for the third amino acid residue of ORP1. The haemin binding protein can be used in vaccines for preventing or treating H. somnus infections, which cause thromboembolic meningo-encephalitis, septicaemia, arthritis and pneumonia in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 199
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-1993;
29-MAR-1993;
                             Pasteurella
                                                                                                                  AAR14482;
                                                                                                                                      AAR14482 standard;
                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           and corresp. DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus somnus immunogenic proteins used in vaccines - selected from haemin-binding protein, haemolysin, LppB and LppC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus somnus; immunogenic; haemolysin; LppB; LppC; thromboembolic meningoencephalitis; septicaemia; arthritis; pneumonia; lktA gene; haemin-binding protein; fusion protein.
                                                  Antigen; leukotoxin; vaccine; lktA
                                                                                             15-JAN-1992
                                                                                                                                                                                                                                                                                                               See also AAR42370-86.
                                                                                                                                                                                                                                                                                                                          vertebrates
                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 5; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYSA-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant leukotoxin peptide
                                                                                                                                                                                         747 ndllhggkgddi 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rioux C,
                                                                                                                                                             13
                                                                                                                                                                                                                 Ν
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1993-351733/44.
DB; AAQ51081.
                                                                                                                                                                                                                NDIFHSGEGDDL
                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RJ,
                                                                                                                                                                                                                                                                                          924 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Theisen
                             haemolytica
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   haemolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SASKATCHEWAN
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfeiffer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0038287.
93US-0038288.
93US-0038719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92US-0865050.
92US-0893424.
92US-0893426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93WO-CA00135
                                                                                                                                                                                                                13
                                                                                                                                        Protein; 926
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                                                                                                                                                                                                                                                63.6%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pontarollo
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                                                                                                                                                                                                                                               Score 49; I
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (split) from plasmid
                                                                                                                                        AA
                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                 DB
5.7;
                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potter
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                                                                                                                                                                                                                                                          Length 924;
                                                                                                                                                                                                                                      Indels
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contg. the gene was ligated into the Smal site of pucil to form pAA179. From this, two constructs were made in the ptac-based vector, pGH432:laci digested with Smal. One, pAA342, consisted of the 5' Ahaili fragment from lktA while the other, pAA345, contained the entire Mael fragment. Clone pAA342 expressed a truncated leukotoxin peptide at high levels while pAA345 expressed full length leukotoxin at very low levels. The 3' end of the lktA gene of pAA345 was therefore ligated to Styl/BamHI digested pAA342 to yleld pAA352 contg. the LKT352 sequence. The protein expressed from the vector can be used to prepare a subunit vaccine with other P. haemolytica antigens, e.g. fimbrial protein, plasmin receptor or 50K outer membrane protein. The vaccines can be used to parte of cattle from the vaccine with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shipping
See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The LKT352 gene was prepd. contg. the gene was ligated paal79. From this, two con
                                                                                                                                                       Vector; LKT 352; flanking; recombinant; antigen; somatostatin;
gonadotropin releasing hormone; rotavirus viral protein 4;
carrier protein; lactation; reproduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccines for Pasteurella haemolytica infection in cattle - comprise sub-unit antigens from P haemolytica fimbrial protein, plasmin receptor, 50 K outer membrane protein and leukotoxin.
                                                                                                                                                                                                                                                                             AAR34545
                                                                                                                                                                                                                                                                                                     AAR34545 standard; Protein; 926 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 5; 92pp; English.
16-OCT-1991;
14-OCT-1992;
                                          15-OCT-1992;
                                                                       29-APR-1993
                                                                                                                             Pasteurella haemolytica
                                                                                                                                                                                                                   Leukotoxin 352 produced from
                                                                                                                                                                                                                                                23-AUG-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to protect cattle from respiratory diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKT352 is 98% homologous with authentic leukotoxin and migrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acres SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-0CT-1991
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                                                                                                                                                                                                                                                                                                                                                                                 747
                                                                                                                                                                                                                                                                                                                                                                                                            N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the same position on gels.
                                                                                                                                                                                                                                                                                                                                                                            ||: | |:|||:
ndllhggkgddi 758
                                                                                                                                                                                                                                                                                                                                                                                                            NDIFHSGEGDDL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 58.: 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fever pneumonia.
AAR14481, 83,84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bariuk LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                926 AA;
91US-0779171.
92US-0960932.
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                                          92WO-CA00449.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as follows: lktA, an MaeI fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49; DB Pred. No. 5.7; 3; Mismatches
                                                                                                                                                                                                                   pAA352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lawman
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12;
5.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MJP;
                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 926;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pneumonia, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                       colonies were screened for their ability to produce leukotoxin by colonies were screened for their ability to produce leukotoxin by colonies were screened for their ability to produce leukotoxin by colonies were screened for their ability to produce leukotoxin by colonies were into the neutrophils. A 4kb crelease of lactate dehydrogenase from the neutrophils. A 4kb creament was obtd. Progressively larger clones were isolated by colonies walking to isolate full length recombinants of ca. 8kb, colonies, one was subjected to restriction enzyme digestion to yield two clones, one expressing truncated leukotoxin peptide at high levels and the other expressing truncated leukotoxin peptide at low levels. The 3' end of the lkt gene from the full length clone was ligated to the truncated gene clone to yield plasmid pha352. The clone was used to produce chimeric proteins by gene fusion with an antigen coding sequence, e.g. the coding sequence of somatostatin, gonadotrophin releasing hormone or rotavirus viral protein 4, i.e. leukotoxin works as a carrier protein to bring about a larger immune response than the antigen alone. Immunisation with these antigens can regulate growth rate, lactation and reproductive efficiency. See also AAR34546-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in lambda gtll and pUCl3. Resulting clones were used to transform E coli and individual colonies were pooled and screened for reaction with serum from a calf which had survived a P. haemolytica infection and that had been boosted with a conc. culture supernatant of P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene libraries of P. haemolytica Al (strain B122) were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 3; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gonadotropin releasing hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprises chimeric protein comprising leuco:toxin peptide homologous protein fused to antigen esp. somatostatin or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunological carrier system with enhanced immunogenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYSA-) UNIV SASKATCHEWAN
926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Redmond MJ
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Ş Matches Query Match Best Local 2 NDIFHSGEGDDL 13 7; Conserv Conservative 58.3%; score 49; DB; Pred. No. 5.7; 3; Mismatches 5.7; 14; Length 926; Indels 0 Gaps

0;

Sequence

RESULT AAR50291 ID XXX AC 밁 06-OCT-1994 AAR50291; AAR50291 standard; Protein; ||: | |:||: | 747 ndllhggkgddi 758 15 (first entry) 926 AA

LKT352. Vaccine; regulated membrane protein; protein; OMP; Haemophilus somnus; leukotoxin; Pasteurella haemolytica; Recombinant leukotoxin from plasmid pAA352

Pasteurella haemolytica Al (strain B122)

03-JAN-1994

29-JUN-1993; 93CA-2099707

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Page 8
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                                                                                                                    Q
                                                                                                                                                                                                                                                                                                                                             A vaccine comprising an outer membrane protein (OMP) extract of Haemophilus somnus enriched with iron regulated proteins is new. The vaccine pref. further comprises an immunogenic leukotoxin polypeptide, esp. an immunogenic pasteurella haemolytica leukotoxin hamologous to LKT352. Example 1.2 describes the prodn. of p. haemolytica recombinant leukotoxin from pAA352.

Two expression constructs were made. One, pAA342, contained the cyrament of the ltkA gene, while the other, pAA345, contained the entire lktA gene, pAA342 expressed a truncated leukotoxin peptide at high levels, while pAA345 expressed full clenth leukotoxin at very low levels. Therefore, the 3' end cof the lktA gene was ligated into pAA342, yielding plasmid pAA352.

LEWT352 or new leukotoxin is 98% homologous to authentic
earch completed: September 11, 2002, 08:58:48
ob time: 192 sec
                                                                                                                                                       Query Match 63.6%;
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus somnus outer membrane protein extract - enriched with iron-regulated proteins, opt. contg. leuco:toxin antigens, for use as vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-092909/12.
N-PSDB; AAQ44760.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harland RJ, Potter AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                              leukotoxin.
NB: the protein sequence in Fig 5 comprises 926 amino acids, however this protein is described in the text as having 931 amino acids.
                                                                                                                                                                                                                                              Sequence
                                                                                     2 NDIFHSGEGDDL 13
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747 ndllhggkgddi 758
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Result
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Listing first 45 summaries
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                                                                                                                                M. bovis Dalton 2d
Leukotoxin 352 ge
Chimeric protein #
Bovine IL-2/Pasteu
GnRH-leukotoxin ge
                                                                                                                                                                                                                                                                                                                                           Description
Leukotoxin 352 gen
Recombinant leukot
                                LKT352 gene. F
Leukotoxin 352
                                                                                                   Rotavirus VP4-leuk
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Nucleic acid encod	AAV61532	19	1635	12.3	341.8	Ç,
Leukotoxin carrier	AAX99361	20	1473		342.4	4
re	AAZ46400	21	2088		•	ω
DNA encoding a leu	AAZ55700	21	2088	•	343.2	N
Nucleic acid encod	AAV61535	19	2088	•	•	1
Pasteurella haemol	AAD08976	22	1359	•	•	0
Enterohaemorrhagic	AAT08098	17	2278	14.5	0	9
LhaA (low homology	AAQ94784	16	3240	•		80
LhaA (low homology	AAQ94783	16	3072	•	•	7
	AAD08975	22	1827	•		σ
A. pleuropneumonia	AAZ88584	21	3762		88	S
ApxICA gene. Acti	AAT73217	18	3762			4
A. pleuropneumonia	AAZ88587	21	7721	•	629	w
ApxIIIABCD gene.	AAT73220	18	7721	•	629	N
Leukotoxin AppIIIA	AAQ64827	15	4008		. 629	יי
appCA region encod	AAQ11873	12	3831	•	773.4	0
A. pleuropneumonia	AAZ88586	21	4731	•	775	ø
ApxIIAB'C gene. A	AAT73219	18	4731	27.8	775	8
P. suis leukotoxin	AAT45417	17	3848		800.4	7
Leukotoxin genes.	AAQ14000	12	4203	•	807.6	σ
P. haemolytica leu	AAT37179	17	2794	•	811.2	ഗ
Somatostatin-leuko	AAQ41321	14	2838	•	812.8	4
Sequence encoding	AAQ06074	11	7183	•	813	ω
Paste	AAQ70050	15	7184	•	814	N
	AAQ46410	14	3879	•	814	_
IL-2/LK	AAQ54212	15	3311	•	814	0
\vdash	AAQ22771	13	3311	•	814	ø
Plasmid pGCH5 whic	AAQ51081	14	3977	•		8
	AAQ51082	14	3887	•	•	7
	AAQ51086	14	3646	•		σ
Bovine gamma-IFN/P	AAA72484	21	3229			5
Chimeric protein #	AAT60033	18	3229	•		4
Bovine IFNgamma/LK	AAQ54213	15	22	•		ω
Nucleic acid encod	6153	19	9	•	814.4	N
-GnRH fusi	71	17	9	•	814.4	
Nucleic acid encod	AAV61530	19	2794	•	814.4	0

ALIGNMENTS

AAF57290 RESULT CDS CDS CDS 31-AUG-2000; 2000WO-AU01048 08-MAR-2001. WO200116172-A1. Moraxella antibacterial; Moraxella; antigen; immune response; infection; RTX toxin; vaccine; antibacterial; ds. M. bovis Dalton 2d RTX toxin A subunit encoding DNA 29-MAY-2001 AAF57290; AAF57290 standard; DNA; 3231 BP _ bovis (first entry) Location/Qualifiers 232..3015 /product= "RTX toxin A subunit" 1..195 /note= "partial coding region of 3080..3250 /*tag= /*tag= "partial coding region of RTX toxin B subunit" σ RTX toxin a subunit"

99AU-0002571

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                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to new Moraxella bovis antigens and nucleic aci sequences encoding these antigenic polypeptides. The antigenic polypeptides and polypucleotides are useful for raising an immune response in an animal directed against Moraxella, preferably against M. bovis or M. catarrhalis, and for treating Moraxella infections. The present sequence represents the nucleotide sequence of the A subunit the RTX toxin from M. bovis Dalton 2d.
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                                                                      ttgattaatgagataattggtaatctatctcagagtactcaaacgattgaagcattttct
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                                                                                                      gattetttaateaaaaaaggtgatgetgeacetgatgetttggetaaagetagtattgae
                                tcacagttagcaaagttaggttctactatatcgcaggctaaaggcttctctaatatagga
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UNIV MELBOURN
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Matches 1530;
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                                                                   attctaccaataagttagccaaagggttagacagtgtagaaaatattgatcgtaaattag
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gtaaagcaagtaatgtattatcaacattaagctcttttttgggcactgcattagcgggta
                                                                                                                                                                                                                        aagaacgcaataatattgcaacagctcaaaccagtttaggcacgattcaaaccgctattg
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Best Local Similarity
Matches 1544; Conser
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22-AUG-1990;
16-OCT-1991;
                                                                   IFN), linked to at least one RTX toxin epitope (preferably the sequence shown in AAWI3865). The RTX toxin used to provide the epitope sequence is preferably a leukotoxin, especially the full-length Pasteurella haemolytica leukotoxin. Alternatively, the leukotoxin is a truncated leukotoxin lacking leukotoxic activity, especially LKT352. The chimeric proteins can be used for the production if vaccines against respiratory diseases such as pneumonia, particularly fibrinous pneumonia caused by P.haemolytica, including shipping fever in cattle.
                                                                                                                                                     AAT60032 and AAT60033 represent the coding sequences for immunogenic chimeric proteins of the invention. This sequence represents a chimeric protein containing the bovine interleukin-2 (II-2) sequence and a leukotoxin sequence. The chimeric proteins of the invention comprise a cytokine, selected from interleukin-2 (II-2) and gamma interferon (gamma cytokine, selected from interleukin-2 (II-2) and gamma interferon
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22-AUG-1990;
16-OCT-1991;
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(CIBA )
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                                          Vaccine for stimulating immunity against pneumonia protein comprising gamma-interferon and leukotoxin Pasteurella haemolytica -
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DB; AAB21073.
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Pasteurella
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90US-0571301.
91US-0777715.
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Best Local Similarity 60.1%;
Matches 1544; Conservative
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Best Local Similarity
Matches 1538; Conserv
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14-OCT-1992;
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Pred. No. 1.3e-170;
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                                                                                                                                                                                                                                                                                                                                         Immunological carrier system with enhanced immunogenicity comprises chimeric protein comprising leuco:toxin peptide homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone
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14-OCT-1992;
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/note= "recombinant
2779..2861
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Pred. No. 1.3e-170;
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                                               The LKT352 gene was prepd. as follows: lktA, an MaeI fragment contg. the gene was ligated into the SmaI site of pUCl3 to form pAA179. From this, two constructs were made in the ptac-based vector, pGH433:lacI digested with SmaI. One, pAA342, consisted of the 5' AhaIII fragment from lktA while the other, pAA345, contained the entire MaeI fragment. Clone pAA342 expressed a truncated leukotoxin peptide at high levels while pAA342 expressed full clength leukotoxin at very low levels. The 3' end of the lktA gene of pAA345 was therefore ligated to Styl/BamHI digested pAA342 to yield pAA352 contg. the LKT352 sequence. The protein expressed from the vector can be used to prepare a subunit vaccine with other P. haemolytica antigens, e.g. fimbrial protein, plasmin of the pAA342 contg. The segment of the vaccines can be used to protect cattle from respiratory diseases such as pneumonia, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccines for Pasteurella haemolytica infection in cattle comprise sub-unit antigens from P haemolytica fimbrial protein, plasmin receptor, 50 K outer membrane protein and leukotoxin.
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	g 976	ttaaaaaattaggctatgacggagataatttattagcagaatatcagcggggaaca	917	DЪ
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	g 883	tactggtgctgttgctgctttaattacttcatcgattatgttggcaattagtcctttg	824	Оy
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	a 823	tqtaacaaaaqcaatttcttcatatqttttaqcacaacqtqttqctqctqqtctatca	764	0
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	a 676	atgttatctcagggctattatcgggcgcaacagctgcacttgtacttgcagata	617	Db
	a 703	ggaaataattactggtttgctatcaggcatttctgcagg	644	Qy
	t: 616	tcggtggacttgataaagctggccttggt	557	Db
	t 643	ctctaatataggaaacaagttgcaaaacttaaatttttctaaaacaaatcttggt	587	Qγ
	t 556	atatcaaaggc	497	рь
	t 586	gaagcattttcttcacagttagcaaagttaggttctactatatcgcaggctaaaggc	527	Qy
	c 496			Db
	a 526	agctagtattgacttgattaatgagataattggtaatctatct	467	Qγ
	a 436	ggaatggatttagatgaggccttacagaataacagcaaccaacatgctcttgct		Db
	1 466	gggtatagaacttgattctttaatcaaaaaaggtgatgctgcacctgatgctttggct	407	Qγ
		gcaaataaagccaaaactgtattatctggcattcaatctattttaggctcagtattg	N	Db
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	346	aaaaacattotaocaataagttagocaaaggttagacagtgtagaaaatattgatogta aaaaacattotaocaataagttagocaaaggttagacagtgtagacagtg 	287 269	Оy
	6	attggcttaactgagcgtggcattgtgttatccgctccacaaattgataaattgcta	0	Db
	28	ctctctcacacaaactggtattgctatttctgcaaca	227	Qy
	3 208	agagaagaacgcaataatattgcaacagctcaaaccagtttaggcacgattc	149	Db
	226	agcctaat	167	Qу
	148	gtaatggtttacaggatttagtcaaagcggccgaagagttgggga	89	Db
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colonies were screened for their ability to produce leukotoxin by incubating cell lysates with bovine neutrophils and measuring the release of lactate dehydrogenase from the neutrophils. A 4kb fragment was obtd. Progressively larger clones were isolated by chromosome walking to isolate full length recombinants of ca. 8kb, in pakilia. The clone was subjected to restriction enzyme digestion to yield two clones, one expressing truncated leukotoxin peptide at high levels and the other expressing truncated leukotoxin at low levels. The 3' end of the lkta gene from the full length clone was suigated to the truncated gene clone to yield plasmid pakis2. The clone was used to produce chimeric proteins by gene fusion with an antigen coding sequence, e.g. the coding sequence of somatostatin, gonadotrophin releasing hormone or rotavirus viral protein 4, i.e. leukotoxin works as a carrier protein to bring about a larger immune response than the antigen alone. Immunisation with these antigens can regulate growth rate, lactation and reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene libraries of P. haemolytica Al (strain B122) were constructed in lambda gtll and gUCl3. Resulting clones were used to transform E coli and individual colonies were pooled and screened for reaction with serum from a calf which had survived a P. haemolytica infection and that had been boosted with a conc. culture supernatant of P.
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[3]

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0; Mismatches 0 4; DB 14; 1.8e-170; 956; Indels Length 2794 60; Gaps 466 496 436 379 406 319 346 268 286 106

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            gttatatcacttccgatcaaattgataaaatttt 2567
                                           tgcctaattataaagcaactaaagatgagaaaatcgaagaaatcatcggtcaaaatggcg
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RESULT
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ВP

06-OCT-1994

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Best Local Similarity 60.2%;
Matches 1538; Conservative
                                                                                                                                                                                                                        Two expression constructs were made. One, pAA342, contained the 5'-AhaII fragment of the ltkA gene, while the other, pAA345, contained the entire lktA gene. pAA342 expressed a truncated leukotoxin peptide at high levels, while pAA345 expressed full length leukotoxin at very low levels. Therefore, the 3' end of the lktA gene was ligated into pAA342, yielding plasmid pAA352. LKT352 or new leukotoxin is 98% homologous to authentic
                                                                                                                                                                                                                                                                                                       polypeptide, esp. an immunogenic Pasteurella haemolytica leukotoxin homologous to LKT352. Example 1.2 describes the prodn. of P. haemolytica recombinant leukotoxin from pAA352.
                                                                                                                                                                                                                                                                                                                                         A vaccine comprising an outer membrane protein (OMP) extract Haemophilus somnus enriched with iron regulated proteins is not the vaccine pref. further comprises an immunogenic leukotoxin
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                   The present sequence represents a recombinantly produced or chemically synthesised nucleic acid encoding leukotoxin 352 (LKT 352), derived from the lktA gene that is present in the plasmid pAA352. This gene produces a truncated protein that has an estimated molecular weight of about 99 kDa and lacks the cytotoxic portion of the molecule. Thus this gene has a higher expression level than that of the full-length molecule. This can be used in the construction of a chimeric protein that comprises a leukotoxin polypeptide, several multimers, and a GRH sequence. The chimeric protein can be used as a vaccine to help reduce the incidence of mammary tumours in a mammalian individual.
                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 multimer; v
cytotoxic;
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multimer; vaccine; tumour;
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incidence
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plasmid pAA352;
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Que Bes Mat	ery Ma st Loca tches	tch 29.3%; Score 814.4; DB 19; Length 27 al Similarity 60.2%; Pred. No. 1.8e-170; 1538; Conservative 0; Mismatches 956; Indels 6	٠.
Оy	53 29	aagtotggattaaaaaatotttacttggctattocccaaagattatgatoc	
VΩ	107	aaggtgggactttaaatgattttattaaagctgctgatgaattaggtattgctcgtt 1 	
В	89	caaggtaatggtttacaggatttagtcaaagcggccgaagagttggggattgag	
Qy	6	agaagagcctaatcacactgaaacagcaaaaaaaatctgttgacacagtaaatcagt	
망	149	agagaagaacgcaataatattgcaacagctcaaaccagtttaggcacgattcaa	
Qy	227	tattgctatttctgcaacaaattagaaaagttcttac 2	
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망	269	gaaaactaaagcaggccaagcattaggttctgccgaaagcattgtacaa	
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В	737	tattaccaaagccgtttcttcttacattttagcccaacgtgttgcagcaggtttatctt 7	
Qγ	824	gctgttgctgctttaattacttcatcgattatgttggcaattagtcctttgg 88	
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DT 24-I
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KW tu Chimera; pCB113; LKT 352; GnRH; Gonadotropin releasing hormone; mulcytotoxic activity; antigen presentation; immune response; vaccine; Synthetic tumour; SS multimer;

Nucleic 24-DEC-1998

acid

encoding (first

entry) LKT-GnRH

Location/Qualifiers 1..2934 /*tag= a

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P-PSDB;
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                                                        ttctctctctcacacaaactggtattgctatttctgcaacaaaattagaaaagttcttac
                                                                                        aaagagaagaacgcaataatattgcaacagctcaaaccagtttaggcacgattcaaaccg
                                                                                                    tagcagaagagcctaatcacactgaaacagcaaaaaaatctgttgacacagtaaatcagt
                                                                                                                                                                               caaaaactggggcaaaaaaattatcctctatattccccaaaattaccaatatgatactg
                                            ctattggcttaactgagcgtggcattgtgttatccgc
                                                                                                                                                                                                                                                                                                                                                                                    3; Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFNgamma/LKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interleukin-2; IL2; P. haemolytica; leukotoxin; LTK;
                                                                                                                                                                                                                                                                                  3229 BP; 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hughes HPA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polyclonal; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heamolytica -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEIGY CANADA LTD SASKATCHEWAN.
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                                                                                                                                                                                                                                                                                                                                                                                    7; 56pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-0571301.
91US-0777715.
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/product=
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-actaaagcaggccaagcattaggttctgccgaaagcattgtacaaa
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                                                                                                                                                                                                                                       29.3%;
                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                  A; 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFNgamma-LKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fusion protein;
tibody; ds.
                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                           Score 814.4; DB 15
Pred. No. 1.9e-170;
D; Mismatches 956;
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                                                                                                                                                                                                                                                                                  690
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                                                                                                                                                                                                                                                                                  883 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; interferon;
                                                                                                                                                                                                                                                 DB 15;
                                             ccacaaattgataaattgctac
                                                                                                                                                                                                                            956;
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                                                                                                                                                                                                                            Gaps
                        346
                                              268
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δõ B δõ Вb ΔÃ Qу Д Qγ DЬ δÃ Вb δÃ qq ν Вb ρ 밁 Qy В Qγ Дb δõ Ъ Qy Вρ Qy Db ŶΩ δ Вр Qγ DЬ В Qy Вþ QY 1424 1304 1217 1244 1157 1184 1097 1124 1037 1064 1004 1277 977 917 944 857 884 824 677 617 644 557 587 797 737 764 704 497 527 437 467 380 407 ctgagctaaataaagagttggaagctgaacgtgttattgcaatcacccaacaacgttggg aagcttatgcagatgcttttgaagatggcaagaaagttgaagctggttccaatattactt ataacaacattggtgatttagctggtattagccgtttaggtgaaaaagtccttagtggta ataataatattggtgagttagcaggtattaccaaattgggtgaacgcattaagagcggaa ctaaccgtttacaaggtaaaattttagagtgggaaaagcaaaatggcggtcagaactatt ttacaggattgatctctggaattttagaagcgtctaaacaggcaatgtttgaaagtgttt ggactattgatgcatcggttactgcaattaataccgcattggccgctattgctggtg gtactattgaagcttcattaactacaattagtacggcattaggtgcagtttctgctggtg aattccgaaaatttggctatgatggggatcatttattggctgaatatcagcgtggtgtgg catttatgaatgcagcagataaattcaatcatgctaatgctcttgatgagtttgcaaaac atgcttcaacagctaaaaaagtgggtgcgggttttgaattggcaaaccaagttgttggta atgcatcgactggcaaaaaagttgctgcaggttttgaattaagcaatcaagttattggta tgaacttaaacaaagagttacaggcagaacgtgtcatcgctattactcagcagcaatggg ttgataaaggctatgattctcgttatgctgcttatttagctaataacttaaaatttttgt tgtctgctgctgcagccggctcggttattgcttcaccgattgccttattagtatctggga tttccgctgctgctgtaggatctgctgttggtgcaccgattgcactattagttgcaggtg gctttaaaaaattaggctatgacggagataatttattagcagaatatcagcggggaacag catttgccggtattgccgataaatttaatcatgcaaaaagtttagagagttatgccgaac caactgggcctgttggctttaattgcttctactgtttctctttgcgattagcccattag tggaaataattactggtttgctatcaggcatttctgcaggctttgctttagcggataaaa ttgaagcattttcttcacagttagcaaagttaggttctactatatcgcaggctaaaggct ttgaaaatggttacgatgcccgttatcttgcgaatttacaagataatatgaaattcttac caaataaaattcataacaaaattgtagaatgggaaaaaaataatcacggtaagaactact ttaccggtgtaatttctacgattctgcaatattctaaacaagcaatgtttgagcacgttg tagatgttatctcagggctattatcgggcgcaacagctgcacttgtacttgcagataaaa tagggactttaggagacaaactcaaaaatatcggtggacttgataaagctggccttggtt ttgacgaatttggtgagcaaattagtcaatttggttcaaaactacaaaatatcaaaggct aagctggcttggagctaacaaattcattaattgaaaatattgctaattcagtaaaaacac ctggaatggatttagatgaggccttacagaa---taacagcaaccaacatgctcttgcta cgggtatagaacttgattctttaatcaaaaaaggtgatgctgcacctgatgctttggcta 1276 1216 1243 1483 1096 1123 1036 1063 1003 976 916 943 856 883 796 823 616 643 496 763 676 703 556 586 436 466 379 406

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QΥ 멍 Qy Дb Qy ДЪ QУ Вb QΥ 뫄 Qγ Вþ δÃ Ъ Qy Db QY Qy Дb 20 밁 멍 Qy Db δÃ В Qy В Qy В Qγ Ър Qy Ъ Qy B 2478 2408 2183 21112051 1943 1874 1817 1757 1697 2423 2351 2291 2303 2231 2171 2123 2063 1934 1883 1823 2003 1724 1637 1577 1457 1397 1664 1604 1517 1544 gcaaaaaagagaaagtgaccattcaaaactggttccgagaggctgattttgctaaagaag atcattcaggtagtattaacataccaagatggtacataacatcaaatttacaaaa.---caaatatatctgatattatgattgaacgtaccaaagagggtattatagttaaacgaaatg gcgatggtaatgatattattaccgattctgacggcaatgataaattatcattctctgatt gtgatggtaatgatactttgtacgatggcacgggcaatgataaattagcatttgcagatg gtaaaggcaacgacctattacacggtggcaagggcgatgatattttcgttcaccgtaaag gttctggtgatgatgtattaaattggtggtgctggtaatgatgtctatatctttcggaaag tattccatagtggtgaaggtgatgatttactcgatggtggtgctggtgacgaccgcttgt gtcatagcaataaccagcaccatg---ccggttattacaccaaagataccttgaaagctg gtgattatgaattaagaaaagttgggtatggttatcagtctaccgataatttgaaatcag acgaagtgacttcaacccataccgcattagtgggcaaccgtgaagaaaaaatagaatatc atgaagttgtgaagcgtcaagaaaccaaggtgggtaaacgtactgaaactatccagtatc aagagaccgagcaaggtagttataccgtaaatcgtttcgtagaaaccggtaaagcactac gtgcaacagaagcaggcagttatacagttaatcgtaaggttgctcgaggtgatatctacc acgatcgtgtcttctatagtaaagacggaggatttggtaatattactgtagatggtacga aaggcacagacgagattggtctaatagtaaatgcaaaa------gtaaatactcttatattaataagttaaaaattcggacgtgtaaaaaactggcaagttacag cgaacttaaaagatttaacatttgaaaaagttaaaca---taatcttgtcatcacgaata ttggtggtaaaggcgatgatattctcgatggtggaaatggtgatgattttatcgatggcg cctttaacggtggtgatggtgtcgatactattgacggtaacgacggcaatgaccgcttat acgaccgagttcactatag---ccgtggaaactatggtgctttaactattgatgcaacca gtaaatatgaatatattaccaagctcaatattaaccgtgtagatagctggaaaattacag tggatgctaaaactggtatcatagacattagtaattcaaatgggaaaaaaacgccaagcgt tagacaatgctggaaatgtaactaaaaccaaagaaacaaaaattattgccaaacttggtg tcttattcagaacgccattattgacgccgggaacagagcatcgtgaacgcgtacaaacag tgcatttcacttcgcctttgttaacagcaggaactgaatcacgttgaacgtttaactaatg tggattcggcaaacggtattattgatgtgagtaattcgggtaaagcgaaaactcagcata ttatcaaagtaataaaacagatcataaaattgagcaactaattggtaaagatggta ģ 2533 2407 2290 2302 2230 2242 2170 2110 2122 2050 2062 1993 2002 1933 1942 1873 1882 1816 1822 1756 1762 1696 1723 1636 1663 1576 1516 1543

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AAT60033
ID AAT600
XX AAT600
XX AAT600
XX Chimer
XX RTX CY
KW Intell
KW Pasteu
KW Fibrin
XX FT CDS
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                      Query Match
Best Local Similarity
Matches 1538; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-1993;
22-AUG-1990;
16-OCT-1991;
                                                                                                                                                                 AAT60032 and AAT60033 represent the coding sequences for immunogenic chimeric proteins of the invention. This sequence represents a chimeric protein containing the bovine gammainterferon (gamma IFN) sequence and a leukotoxin sequence. The chimeric proteins of the invention comprise a cytokine, selected from interleukin-2 (IL-2) and gamma IFN, linked to at least one RTX toxin epitope (preferably the sequence shown in AAW13865). The RTX toxin used to provide the epitope sequence is preferably a leukotoxin, especially the full-length Pasteurella haemolytica leukotoxin. Alternatively, the leukotoxin is a truncated leukotoxin activity, especially LKT352. The chimeric proteins can be used for the production if vaccines against respiratory diseases such as pneumonia, particularly fibrinous pneumonia caused by P. haemolytica, including shipping fever in cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTX cytotoxin; cytokine; immunogen; chimeric protein; cytokine; interleukin-2; IL-2; gamma interferon; gamma IFN; leukotoxin; p: Pasteurella haemolytica; LKT352; respiratory disease; shipping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT60033
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                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic
toxin - usef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CIBA ) CIBA
(UYSA-) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW13867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unic chimeric proteins comprising useful in vaccines, esp. against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                               3229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hughes HPA,
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEIGY CANADA LTD SASKATCHEWAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytokine;
IL-2; gamm
                                                                                                                               B₽;
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90US-0571301.
91US-0777715.
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                                        29.3%;
60.2%;
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                                                                                                                               571 C;
                        0;
                      Score 814.4; DB 18
Pred. No. 1.9e-170;
0; Mismatches 956;
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                                                                   DB 18;
                                                                                                                               T; 0
                        Indels
                                                                   Length 3229;
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                        60;
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pneumonia;
                        Gaps
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22-JUL-1996;
22-AUG-1990;
        Vaccine for stimulating immunity against pneumonia protein comprising gamma-interferon and leukotoxin Pasteurella haemolytica -
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                                                                                                                                       16-OCT-1991;
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2528 agcggatcacctcaaagcaagttgatgatcttat 2561
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RESULT
AAR10889
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Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-APR-1990;
                                                                                                                               AAR42385
                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                    vaccines to protect cattle from respiratory diseases. They can also be used to produce antibodies for immunoaffinity purifice. of further proteins. [Fig. confg. sequence v. poor].
See also AAR10890, AAR10909, AAR10910 and AAO10783.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; Fig 5; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pasteurella haemolytica proteins vaccines to protect animals esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1991-000097/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYSA-) UNIV SASKATCHEWAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA2014033-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pasteurella haemolytica Al strain B122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKT; vaccine; antigen; respiratory disease; shipping fever pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leukotoxin 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-APR-1991
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                    Pasțeurella haemolytica
                                                                                                                                                    AAR42385 standard; Protein;
WO9321323-A
                                         pneumónia; lktA gene; haemin-binding
                                                    Haemophilus somnus; \mmunogenic; haemolysin; LppB; LppC; thromboembolic meningOencephalitis; septicaemia; arthritis;
                                                                                    Recombinant
                                                                                                          19-APR-199
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|422 fllnlnkelgae 433
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9; Conserv
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                                                                                                                                                                                                                                                                                                                 924 AA;
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                                                                                    leukotoxin peptide from plasmid
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75.0%;
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Pred. No.
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                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and genes - used for producing cattle from respiratory diseases
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                                          protein; fusion protein
                                                                                                                                                                                                                                                                  DB
52;
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04-JUN-1992;
29-MAR-1993;
29-MAR-1993;
09-APR-1992;
04-JUN-1992;
04-JUN-1992;
04-JUN-1993;
29-MAR-1993;
29-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The lppB gene protein was expressed in E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene iktA coded for by plasmid pAa352. The llpB gene fragment was taken from pMS11. LppB can be used in vaccines for preventing or treating H. somnus infections, which cause thromboembolic meningo-encephalitis, septicaemia, arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus somnus immunogenic proteins used in vaccines selected from haemin-binding protein, haemolysin, LppB and LppC,
                                                                                                                                                    Haemophilus somnus; immunogenic; haemolysin; Lpp8; LppC;
thromboembolic meningoencephalitis; septicaemia; arthritis;
pneumonia; lktA gene; haemin-binding protein; fusion protein
                                                                                                                                                                                                                                                                    AAR42380 standard; Protein; 924 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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                                                                                                                                                                                               Recombinant leukotoxin peptide (split) from plasmid pGCH4
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nes 9; Conserv
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fllnlnkelgae 435
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                                                                                                                                 haemolytica.
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heisen M;
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92US - 0865050.
92US - 0893424.
92US - 0893426.
92US - 0893426.
93US - 0038287.
93US - 0038288.
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92US-0893426.
93US-0038287.
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93US-0038719
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52;
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2784
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AZ548467 ENTEK30TR
AZ551618 ENTDV34TR
AZ551092 ENTFD23TF
AZ546009 ENTFW53TF
AZ196050 SP_1031_A
AZ550256 ENTEV58TR
BH149983 ENTOV39TF
AL166032 Tetraodon
AZ528485 ENTCM64TF
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         BH149983
AL166032
AZ528485
AZ676218
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BH160272
AZ535744
         ENTQV49TR
ENTCQ25TR
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AUTHORS
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Contact: Bahrani-Mougeot FK
Department of Medicine-Division of Infectious Diseases
University of Maryland
MSTF Rm 9.00 -10 S. Pine St., Baltimore, MD 21201, USA
Tel: 410-706-7560
Fax: 410-706-8700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bahrani-Mougeot, F.K., Pancholi, S., Daoust, M. and Donnenberg, M.S. Identification of putative urovirulence genes by subtractive
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2b11-593, DNA seguence.
AF307787
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                                                                /db_xref="taxon:562"
/dlone="2b11-593"
/clone="1b="Escherichia coli CFT073"
/clone="ib="Escherichia coli CFT073"
/note="uropathogenic; isolated based on subtractive hybridization with Escherichia coli K12; putative urovirulence genes"
a 61 c 122 g 121 t 4 others
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/strain="CFT073"
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Contact: Bahrani-Mougeot FK
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MSTF Rm 9.00 -10 S. Pine St., Balti
Tel: 410-706-7560
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/note="uropathogenic; isolated based
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ENTEK30TR Entamoeba histolytica
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Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
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quality sequence stop:
Location/Qualifiers
/clone_lib="Entamoeba histolytica Sheared DNA"
note="Vector: pHOS1; Site_l: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
                                                                                                                                             /strain="HM1:IMSS"
/db_xref="taxon:5759"
                                                                                                                                                                                 /organism="Entamoeba histolytica"
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genomic,
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ENTDV54TR Entamoeba histolytica
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              DNA sequence
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Pred. No. 1.7e-06;
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
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Class: shotgun
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Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
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/note="Vector: pHOS1; Site_1: Btf I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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/db_xref="taxon:5759"
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Pred. No. 5.5e-06;
0; Mismatches 372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences HM1: IMSS sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: bjloftus@tigr.org
Clones are derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Brendan J Loftus
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301 838 3543
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quality sequence stop: 829
Location/Qualifiers
                                                                                                                      /db_xref="taxon:5759"
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/clone_lib="Vector: pHOS1; Site_1: Bst I; Constructed at The
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
                                       method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for
                        whole
Sequencing: A Practical Approach,
                                                                                                                                                                                                                                                                                             /strain="HM1:IMSS"
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                                                                                                genomic,
AZ551092
                                                                                                                  912 bp ENTFJ22TF Entamoeba histolytica
1 (bases 1 to 912)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences
HMI: LMSS sheared DNA library
                                           Eukaryota; Entamoebidae; Entamoeba
                                                      Entamoeba histolytica
Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockvilla
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
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/note="vector: pHOS1; Site_1: Bst ; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytic
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (193) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="HM1:IMSS"
/db_xref="taxon:5759"
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Pred. No. 1.2e-05;
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 849)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences
HM1:IMSS sheared DNA library
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AZ546009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: bjloftus@tigr.org Clones are derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
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                                                                                                                     whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin an Barell, Oxford University Press, 1999)."

236 c 43 g 371 t
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/note="Vector: pHOS1; Site_1: Bst I; Constructed at T
Institute for Genomic Research ("TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E, histol
                                                                                                                                                                                                                                                                                                                       using a method described by Clark and Diamond (Clark,
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Entamoeba histolytica"
/strain="HM1:IMSS"
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                2.7%;
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SP_1031_A2_E05_SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus penomic clone Plate=1031 Col=10 Row=I, DNA sequence.

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AZ196050.1 GI:8389873

GSS.
                                                                                                                                                                                                                                                                                 Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. ar
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                               Strongylocentrotus purpuratus.
                                                                          Email: acameron@caltech.edu
Plate: 1031 row: I column
                                                                                                      Tel: (626) 395-8421
Fax: (626) 793-3047
                                                                                                                                          California Institute of Technology
Pasadena California 91125, USA
                                                                                                                                                                      Division of Biology 156-29
                                                                                                                                                                                       Contact: Cameron, RA, Davidson, EH,
                                                                                                                                                                                                                                      additional resources
                                                                                                                                                                                                                                                    A sea urchin genome project: Sequence scan, virtual map,
                                            Seq primer: SP6
Class: BAC ends
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quality sequence stop: 726.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGATGATGACGATGATGATGGTGATGATGACGATGATAACTTTCATCATGTATAATG
                                                                  Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 8208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba
                                                                                                                                                                                                                                                                                                                    genomic, DNA sequence.
AZ550256
AZ550256.1 GI:11175557
                                                                                                                                                                                                    Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 905)

Loftus,B., Van Aken,S. and Fraser,C.
Determination of clone end sequences
HM1:IMSS sheared DNA library
                                                                                                                                                                                                                                                                                                                                                              AZ550256 905 bp
ENTEV58TR Entamoeba histolytica
                                                                                                                                                                                                                                                                           Entamoeba histolytica
High quality sequence start: High quality sequence stop:
                            Seq primer: M13-Reverse
Class: shotgun
                                                                                                                                                                         Contact: Brendan J Loftus
                                                                                                                                                                                     Unpublished (2000)
                                                                                                                                                                                                                                                                                       Entamoeba histolytica.
                                                         DNA library
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ilarity 49.5%;
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DH10B"
a 210 c 64 g
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/clone_lib="Strongylocentrotus purpuratus,
urchin, sperm genomic BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
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Pred. No. 9.7e-05;
0; Mismatches 194;
                                                                        Entamoeba histolytica HM1:IMSS
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                     gggcaatgataaattagcatttgcagatgcaaat 2367
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                                                                                       tggtaatgatgtctatatctttcggaaaggtgatggtaatgatactttgtacgatggcac
                                                                                                                                               agatgaaggcgatgatttactcgatggcggttctggtgatgatgtattaaatggtggtgc
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/note-"Vector: pHOS1; Site_l: BSt I; Constructed at The
/notte-"Vector: pHOS1; Site_l: BSt I; Constructed at The
/nstitute for Genomic Research (TIGR); Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
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Pred. No. 0.00012;
0; Mismatches 378;
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Matches 305;
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aggttgctcgaggtgatatctaccatgaagttgtgaagcgtcaagaaaccaaggtgggta 1978
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Clones are derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Eukaryotic Genomics
The Institute for Genomic Research
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Similarity 44.08;
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/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
Bsing a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. '(193) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
the conservation convencing a protects.
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Entamoeba histolytica
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Pred. No. 0.0002;
0; Mismatches 388;
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             Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a scale clone-end sequencing project of the Tetraodon nigrovirid genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Billault,A., Quetier,F., Saurin,W., Bernot,
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ENTCM64TF Entamoeba histolytica
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The Institute for Genomic Researc
                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Brendan J Loftus
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                                                                                                                                                                                                                                                                                                      Email: bjloftus@tigr.org
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/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytic
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.) The DNA was mechanically sheared to give a
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/db_xref="taxon:99883"
/clone="194G01"
/clone_11b="G"
/clone_1ib="G"
/note="Genoscope sequence ID : COAV
197 c 95 g 117 t 8
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               Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 823)
Loftus B., Van Aken.S. and Fraser.C.
Determination of clone end sequences 1
HM1: IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                     AAACAAAATGTCAAAAAAATCCAAACTATTAAAAAATTAGATAACATTAGATTACCAAGA
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ENTKE36TR Entamoeba histolytica
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Department of Eukaryotic Genomics
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Pred. No. 0.00044;
0; Mismatches 331;
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GACGATGATGATGACGATGAATATGAATATGAATTAGAAGATGAAGAAGCCCCCAAAAAT 243
                                        acgggcaatgataaattagcatttgcagatgcaaatatatctgatattatgattgaacgt 2391
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Similarity 44.8%;
69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_l: BSt I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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/db_xref="taxon:5759"
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Pred. No. 0.00045;
0; Mismatches 331;
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genomic, DNA sequence.
BH139532
BH139532.1 GI:15098593
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                                    gtgggtaaacgtactgaaactatccagtatcgtgattatgaattaagaaaagttgggtat 2031
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TATGATGAAATCGAATTAGAAGAAAATGGTAACGAAGAAGAAAATAACGTGGAATACGAA
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Fax: 301 838 3543
Email: bjloffus@tigr.org
Clones are derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loftus, B., Wang, Z., Van Aken, S. and Fraser, C. Determination of clone end sequences from Entamoeba histolytica HM1: IMSS sheared DNA library (2001)
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High quality sequence stop: 714.
Location/Qualifiers
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Medical Center Dr., Rockville,
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nilarity 44.8%;
Conservative
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/ Clone_lib="Entamoeba histolytica Sheared DNA"
/ Clone_lib="Entamoeba histolytica Stelle, MD.
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.

77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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/strain="HM1:IMSS"
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Pred. No. 0.00045;
0; Mismatches 331;
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Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library (2001)
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Seq primer: M13-Reverse
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/Clone_lib**Entamoeba histolytica Sheared DNA**
/clone_lib**Entamoeba histolytica Sheared DNA**
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
/nstitute for Genomic Research (TIGR), Rockville, MD.
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
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Best Local Similarity 45.0%;
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                              2272 gctggtaatgatgtctatatctttcggaaaggtgatggtaatga 2315
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611 GATGATGAAGATGATGAAGATGAAGATGAAGATGATGA
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Pred. No. 0.00046;
0; Mismatches 321; Indels 0
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   Issued_Patents_NA:*

| (gg12_6/ptodata/2/ina/5A_COMB.seq:*
| (gg12_6/ptodata/2/ina/5B_COMB.seq:*
| (gg12_6/ptodata/2/ina/6A_COMB.seq:*
| (gg12_6/ptodata/2/ina/6B_COMB.seq:*
| (gg12_6/ptodata/2/ina/6B_COMB.seq:*
| (gg12_6/ptodata/2/ina/backfiles1.seq:*
| (gg12_6/ptodata/2/ina/backfiles1.seq:*
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Com
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US-08-455-970A-11

US-08-455-970A-9

US-08-455-970A-9

US-08-455-970A-13

US-08-455-970A-13

US-08-455-970A-13

US-08-694-865-7

US-08-694-865-7

US-08-694-865-7

US-08-17-715-8

US-08-17-715-8

US-08-18-18-3

US-08-18-18-3

US-08-19-18-3

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US-08-19-18-7
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US-08-170-126-1

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US-07-960-932-1

US-07-960-253-1

US-08-455-970A-1

US-08-455-970A-1

US-08-694-865-5

US-08-694-865-5

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STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
OCATION: 1.3294
US-07-777-715-6
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US-07-777-715-6
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 Query Match
Best Local Similarity
Matches 1544; Conserv
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TELEX: 706141
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CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/777,715
FILING DATE: 19911016
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RODINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 29310-2001320
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELECOMMUNICATION 115-327-7250
                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, &
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Campos, Manuel
APPLICANT: Hughes, Huw P.A.
TITLE OF INVENTION: CYTOKINE-LEUKOTOXIN GENE FUSIONS
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 9
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Score 815.6; DB 1;
Pred. No. 1.6e-177;
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                                                                    REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                           APPLICATION NUMBER: PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CAMPOS, MANUEL
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: CYTOKINE-CYTOTOXIN GENE FUSIONS
TITLE OF INVENTION: THEREOF
                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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   MOLECULE TYPE:
            TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: 1in
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CITY: PALO ALTO
STATE: CALIFORNIA
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Best Local Similarity
Matches 1544; Conserva
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              tgagtttgcaaaacaattccgaaaatttggctatgatgggggatcatttattggctgaata
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Pred. No. 1.6e-177;
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APPLICANT: POTTER, ANDREW
APPLICANT: CAMPOS, MANUEL
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: CYTOKIN
TITLE OF INVENTION: THEREOF
                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/170
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07,
APPLICATION INFORMATION:
NAME: ROBINS, ROBERTA L.
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                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                         ZIP: 94301
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 901
TELECOMMUNICATION INFORMATION:
                                                                                                                                            APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
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: TELEFAX: (415) 327-3231
: INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3311 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLFFITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 29.3%;
Best Local Similarity 60.1%;
Matches 1544; Conservative
                                                                                                                                                                               1119
                                                                                                                                                                                                                                          1059 AAATATCAAAGGCTTAGGGACTTTAGGAGACAAACTCAAAAATATCGGTGGACTTGATAA
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810 tgctggtctatcaactactggtgctgttgctgctttaatttacttcatcgattatgttggc
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                                                                                                                                                                          CCAAGTTGTTGGTAATATTACCAAAGCCGTTTCTTCTTACATTTTAGCCCAACGTGTTGC
                                                                 tcaagttattggtaatgtaacaaaagcaatttcttcatatgttttagcacaacgtgttgc
                                                                                                              ACTTGCAGATAAAAATGCTTCAACAGCTAAAAAAGTGGGTGCGGGTTTTGAATTGGCAAA
                                                                                                                               tttagcggataaaaatgcatcgactggcaaaaaagttgctgcaggttttgaattaagcaa
                                                                                                                                                                                                                                                                                                          TTCAGTAAAAACACTTGACGAATTTGGTGAGCAAATTAGTCAATTTGGTTCAAAACTACA 1058
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Pred. No. 1.6e-177;
0; Mismatches 964;
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AAC 2435	tgtagatgtacgagtgcaacagaagcaggcagttatacagttaatcgtaaggttgct	2376	ОУ
237	GGCGGTGAAGGTTACGACCGAGTTCACTATAGCCGTGGAAACTATGGTGCTTT	(A)	Db
98	gatggacacgatcgtgtcttctatagtaaagacggaggatttggtaatat	.80	Qy
3A 231	GCCAAACTTGGTGAAGGTGATGACAACGTATTTGTTGGTTCTGGTAC	25	Db
tga 180	gctqqcaatqacqatatcttqqtqqtcaaqqtaaaatqa	76	ΟV
Ā	TGAATTAGACAATGCTGGAAATGTAACTAAAACCAAAGAAAAAT	2199	Db
1761	gtayccyagacagaagycacagacgagattggtctaatagtaaatgcaaa	1710	Qy
GCG 2198	CTGGAAAATTACAGATGGTGCAGCAAGTTCTACCTTTGATTTAACTAAC	2139	Db
	gcaagttacagatggagaggctagttctaaattagatttctc	1650	Qy
TAG 2138	ACGCGTACAAACAGGTAAATATGAATATTACCAAGCTCAATATTAACCGTGTAGATA	2079	Дb
aaa 1649	cgtttaactaatggtaaatactcttatattaataagttaaaattcggacgtgtaaaa	1590	Qy
TGA 2078	GAAAACTCAGCATATCTTATTCAGAACGCCATTATTGACGCCGGGAACAGAGCATCGTGA	2019	Db
tga 1589	acycaaycyttycatttcacttcycctttyttaacaycayyaac	1530	Оу
AGC 2018	TAAATTAGTACAGTTGGATTCGGCAAACGGTATTATTGATGTGAGTAATTCGGGTAAAGC	1959	Db
gaa 1529	tccaatattactttggatgctaaaactggtatcatagacattagtaattca	1470	Оу
()	GGTAAAGCCTATGTGGATGCGTTTGAAGAAGGCAAACACATTAAAGC	8	Db
tgg 1469	cattaagagcggaaaagcttatgcagatgcttttgaagatggcaagaaagttgaagct	1410	Qy
GAAAA 1898	GTGATTTAGCTGGTATTAGCCGTTTAGGT	8	Db
acg 1409	aacaacgttgggataataatattggtgagttagcaggtattaccaaattgggtç	w	Оу
11 TAC 1838		1779	Db
cac 1349	aaatttttgtctgagctaaataaagagttggaagctgaacgtgttattgcaatc	1290	Qy
TAA 1778	CGGTAAGAACTACTTTGAAAATGGTTACGATGCCCGTTATCTTGCGAATTTACAAGAT	1719	Db
Ba 12	gtcagaactattttgataaaggctatgattctcgttatgctgcttatttagctaat	2	Qy
TCA 1718	GTTTGAGCACGTTGCAAATAAAATTCATAACAAAATTGTAGAATGGGAAAAAAAA	1659	Db
12	tttgaaagtgttgctaaccgtttacaaggtaaaattttagagt	17	Qy
AAT 1	ATTAGTATCTGGGATTACCGGTGTAATTTCTACGATTCTGCAATATTCTAAACAAGCA	1599	DЬ
aat 11	ttgcaggtgttacaggattgatctctggaattttagaagcgtctaaacagg	\vdash	Qy
3CCTT 1598	TATTGCTGGTGGTGTCTGCTGCTGCAGCCGGCTCGGTTATTGCTTCACCGATTGCC	1539	Db
ш	:ttccgctgctgctgtaggatctgctgttggtgcaccgatt	0	Оу
CGC 1538	TCAGCGGGGAACAGGGACTATTGATGCATCGGTTACTGCAATTAATACCGCATTGGCC	1479	Db
tgc 1049	aagcttcattaactacaattagtacggcattagg	990	Qy
SAATA 1478	GAGTTATGCCGAACGCTTTAAAAAATTAGGCTATGACGGAGATAATTTATTAGCAGAA	1419	Db
ata 989	aaaacaattoogaaaatttggctatgatgggggatcatttattggcto	930	Qy
 AGA 1418	CGGTATTGCCGATAAATTTAATCATGCAAAAAGTTT	1359	Дb
Ġ	teetttggeatttatgaatgeageagataaatteaateatgetaatgetet	870	Qy
TGC 1358	${\tt AGCAGGTTTATCTTCAACTGGGCCTGTGGCTTTAATTGCTTCTACTGTTTCTCTTGC}$	1299	Db

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ATTORNEY/AGENT INFORMATION:

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US-07-960-932-1

; Sequence 1, Application US/07960932

; Patent No. 5422110
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APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
TITLE OF INVENTION: CHIMERAS
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                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSEE: ROBERTA L. ROBINS
STREET: 635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2970
                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                         COUNTRY:
ZIP: 943
                                                                                                                                                                                                              STREET:
CITY: P
STATE:
FILING DATE: 1 CLASSIFICATION:
                APPLICATION NUMBER: US/07/960,932 FILING DATE: 19921014
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; LOCATION:
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Best Local
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INFORMATION FOR SEQ ID NO:
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ACTERISTICS:

2794 base pairs

LYPE: NUCLEIC ACID

STRANDEDNESS: do:

TOPOLOGY:

VOLECUI-P

POLECUI-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                             ATGCTTCAACAGCTAAAAAAGTGGGTGCGGGTTTTGAATTGGCAAACCAAGTTGTTGGTA
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Pred. No. 2.9e-177;
0; Mismatches 956;
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acgatcgtgtcttctatagtaaagacggaggatttggtaatattactgtagatggtacga
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                                                                                                     atggagaggctagttctaaattagatttctctaaagttattcagcgtgtagccgagacag
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	34 gttatatcacttccgatcaaattgataaaatttt 2567	2534	Qy
2527	TGCCTAATTATAAAGCAACTAAAGATGAGAAAATCGAAGAAATCATCGGTCAAAATGGCG	2468	Вb
2533	ttatcaaagtaataaaacagatcataaaattgagcaactaattggtaaagatggta	2478	Qy
2467	GCAAAAAAGAGAAAGTGACCATTCAAAACTGGTTCCGAGAGGCTGATTTTGCTAAAGAAG	2408	рь
2477	atcattcaggtagtattaacataccaagatggtacataacatcaaaatttacaaaa	2423	Qy
2407	CGAACTTAAAAAGATTTAACATTTGAAAAAGTTAAACATAATCTTGTCATCACGAATA	2351	망
2422	caaatatatctgatattatgattgaacgtaccaaagagggtattatagttaaacgaaatg	2363	Qy
2350	GCGATGGTAATGATATTATTACCGATTCTGACGGCAATGATAAATTATCATTCTCTGATT	2291	DЬ
2362	gtgatggtaatgatactttgtacgatggcacgggcaatgataaattagcatttgcagatg	2303	Qy
2290	GTAAAGGCAACGTATTACACGGTGGCAAGGGCGATGATATTTTCGTTCACCGTAAAG	2231	Db
2302	gttctggtgatgatgtattaaatggtggtgctggtaatgatgtctatatctttcggaaag	2243	Qy
2230	TTGGTGGTAAAGGCGATGATATTCTCGATGGTGGAAATGGTGATTTTTATCGATGGCG	2171	Db
2242	ttggtggtaaaggcaacgatcgactttctggagatgaaggcgatgatttactcgatggcg	2183	Qy
2170	CCTTTAACGGTGGTGATGGTGTCGATACTATTGACGGTAACGACGGCAATGACCGCTTAT	2111	DЬ
2182	tattccatagtggtgaaggtgatgatttactcgatggtggtggtggtggtgaccgcttgt	2123	Qy
2110	TTGAAGAATTATCGGTACATCACATAACGATATCTTTAAAGGTAGTAAGTTCAATGATG	2051	Б
2122	tagaagaagtaattggttctcaatttaatgatgtattcaaaggttctaaattcaacgaca	2063	Qy
2050	GTCATAGCAATAACCAGCACCATGCCGGTTATTACACCAAAGATACCTTGAAAGCTG	1994	DЬ
2062	gtgattatgaattaagaaaagttgggtatggttatcagtctaccgataatttgaaaatcag	2003	Qy
1993	ACGAAGTGACTTCAACCCATACCGCATTAGTGGGCAACCGTGAAGAAAAAATAGAATATC	1934	Дb
2002	atgaagttgtgaagcgtcaagaaaccaaggtgggtaaacgtactgaaactatccagtatc	1943	Qy
1933	AGAGACCGAGCAAGGTAGTTATACCGTAAATCGTTTCGTAGAAACCGGTAAAGCACTAC	1874	DЬ
1942	gtgcaacagaagcaggcagttatacagttaatcgtaaggttgctcgaggtgatatctacc	1883	Qy
1873	17 ACGACCGAGTTCACTATAGCCGTGGAAACTATGGTGCTTTAACTATTGATGCAACCA 1873	1817	DЬ

RESULT 5
US-07-908-253-1
US-07-908-253-1
; Sequence 1, Application US/07908253
; Patent No. 5534256
; GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: POTTER, ANDREW A.
APPLICANT: POTTER, ANDREW A.
APPLICANT: PARLAND, RICHARD J.
TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L. ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
COUNTRY: UNITED STATES OF AMERICA
COUNTRY: DAIO ALTO
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

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; LOCATION:
US-07-908-253-1
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Best Local Similarity
Matches 1538; Conserv
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INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 2794 base pairs
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REFIERATION NUMBER: 33,208
REFIEROCE/DOCKET NUMBER: 9000-0026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
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APPLICATION NUMBER: US
FILING DATE: 19920702
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CLASSIFICATION:
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atgcatcgactggcaaaaaagttgctgcaggttttgaattaagcaatcaagttattggta
                                    TAGATGTTATCTCAGGGCTATTATCGGGCGCAACAGCTGCACTTGTACTTGCAGATAAAA
                                                          tggaaataattactggtttgctatcaggcatttctgcaggctttgctttagcggataaaa
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Pred. No. 2.9e-177;
0; Mismatches 956;
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Gaps

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US-08-455-970A-1
                                                                                                                                                                                                                                      Sequence 1, Application US/08455970A Patent No. 5708155 GENERAL INFORMATION:
                                                                                        APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P. A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
TITLE OF INVENTION: CHIMERAS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
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STATE: CALIFORNIA
COUNTRY: UNITED STATES OF
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
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                                               TTGACGAATTTGGTGAGCAAATTAGTCAATTTGGTTCAAAACTACAAAATATCAAAGGCT
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; Sequence 5, Application US/08387156
; Patent No. 5723129
; GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
; APPLICANT: HUGHES, HUW P.A.
; APPLICANT: HUGHES, HUW P.A.
; TITLE OF INVENTION: GRRH-LEUKOTOXIN CH

CHIMERAS

RESULT 7 US-08-387-156-5

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REFERENCE/DOCKET NUMBER: 9001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.3%;
Best Local Similarity 60.2%;
Matches 1538; Conservative
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APPLICATION NUMBER: US 07/960,932

APPLICATION NUMBER: US 07/960,932

PRIOR APPLICATION DATA:

APPLICATION UNMBER: US 07/779,171

APPLICATION UNMBER: US 07/779,171

APPLICATION HOMBER: US 07/779,171

APPLICATION NUMBER: US 07/779,171
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION US/OB/387,156
FILING DATE: 10-FEB-1995
CLASSIFICATION: 424
CLASSIFICATION: 424
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ADDRESSEE: REED & ROBINS
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CITY: PALO ALTO
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1423	aatattggtgagttagcaggtattaccaaattgggtgaacgcattaagagcggaa	1364	Qy	
1336	rece 1	1277	дb	
1363	gttggg 1	1304	Qy	
1276	TTGAAAATGGTTACGATGCCCGTTATCTTGCGAATTTACAAGATAATATGAAATTCTTAC 1	1217	дb	
1303	tgataaaggctatgattctcgttatgctgcttatttagctaataacttaaaatttttgt 1	1244	Qy	
1216	ACAAAATTGTAGAATGGGAAAAAAATAATCACGGTAAGAACTACT 1	1157	ДĎ	
1243	cgtttacaaggtaaaattttagagtgggaaaagcaaaatggcggtcagaactatt l	1184	Оу	
1156	TTACCGGTGTAATTTCTACGATTCTGCAATATTCTAAACAAGCAATGTTTGAGCACGTTG 1	1097	ф	
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1096	GCTGCAGCCGGCTCGGTTATTGCTTCACCGATTGCCTTATTAGTATCTGGGA 1	1037	dd	
1123	tccgctgctgctgtaggatctgctgttggtgcaccgattgcactattagttgcaggtg 1	1064	Qy	
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1063	tactattgaagetteattaactacaattagtacggeattaggtgeagtttetgetggtg 1	1004	Qy	
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1003	gggatcatttattggctgaatatcagcgtggtgtgg 1	944	Оу	
)16	AGAGTTATGCCGAAC 9	857	Db	
343	atttatgaatgcagcagataaattcaatcatgctaatgctcttgatgagtttgcaaaac 9	884	Оу	
356	TCTCTTGCGATTAGCCCATTAG 8	797	Db	
383	tactggtgctgttgctgctttaattacttcatcgattatgttggcaattagtcctttgg 8	824	ν	
796	ATATTACCAAAGCCGTTTCTTCTTACATTTTAGCCCAACGTGTTGCAGCAGGTTTATCTT 7	737	ДD	
323	gtaacaaaagcaatttottoatatgttttagcacaacgtgttgctgctggtotatcaa 8	764	νQ	
736	ATGCTTCAACAGCTAAAAAAGTGGGTGCGGGTTTTGAATTGGCAAACCAAGTTGTTGGTA 7	677	Db	
763	tycatcyactygcaaaaaayttyctycayyttttyaattaaycaatcaayttattyyta 7	704	Оу	
576	TGTTATCTCAGGGCTATTATCGGGCGCAACAGCTGCACTTGTACTTGCAGATAAAA 6	617	Db	
703	gaaataattactggtttgctatcaggcatttctgcaggctttgctttagcggataaaa 7	644	Qy	
516	TAGGGACTTTAGGAGACAAACTCAAAAATATCGGTGGACTTGATAAAGCTGGCCTTGGTT 6	557	Db	
543	gtt 6	587	Qy	
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586	aagcattttcttcacagttagcaaagttaggttctactatatcgcaggctaaaggct 5	527	Оу	
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RESULT 8
US-08-694-865-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2794 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                  Matches 1538;
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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REFERENCE/DOCKET NUMBER: 9001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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APPLICANT: MANNS, JOHN G.
TITLE OF INVENTION: GRRH-LEUKOTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: MCCRACKEN, THOMAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 285 HAM CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                aaaaaggtgggactttaaatgattttattaaagctgctgatgaattaggtattgctcgtt 166
                                                                                                                                                                                                                                                                                                                               CAAAAACTGGGGCAAAAAAATTATCCTCTATATTCCCCCAAAATTACCAATATGATACTG 88
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                 aattaggtaaagcaagtaatgtattatcaacattaagctctttttttgggcactgcattag
                                                                                                                              CTATTGGCTTAACTGAGCGTGGCATTGTGTTATCCGCTCCACAAATTGATAAATTGCTAC
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ATGCAAATAAAGCCAAAACTGTATTATCTGGCATTCAATCTATTTTAGGCTCAGTATTGG
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Pred. No. 2.9e-177;
0; Mismatches 956;
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1543	tggatgctaaaactggtatcatagacattagtaattcaaatgggaaaaaaacgcaagcgt	1484	Qy
1456	AAGCCTATGTGGATGCGTTTGAAGAAGGCAAACACATTAAAGCCGATAAATTAGTACAGT	سأ	망
	agcttatgcagatgcttttgaagatggcaagaaagttgaagctggttccaatattactt		Qy
1396	ATAACAACATTGGTGATTTAGCTGGTATTAGCCGTTTAGGTGAAAAAGTCCTTAGTGGTA	1337	В
1423	aataatattggtgagttagcaggtattaccaaattgggtgaacgcattaagagcggaa	1364	Qy
1363	ctgagctaaataaagagttggaagctgaacgtgttattgcaatcacccaacaacgttggg	1304	DB Q9
27	TTGAAAATGGTTACGATGCCCGTTATCTTGCGAATTTACAAGATAATATGAAATTCTTAC	. 21	Дb
0	ttgataaaggctatgattctcgttatgctgcttatttagctaataacttaaaatttttgt	.24	, V
1216	AATAAAATTCATAACAAAATTGTAGAATGGGAAAAAAATAATCACGGTAAGAACTACT	1157	В
1243	taaccgtttacaaggtaaaattttagagtgggaaaagcaaaatggcggtcagaactatt	1184	δõ
1156	ATATTCTAAACAAGCAATGTTTGAGCACGTTG	1097	Ър
1183	tacaggattgatctctggaattttagaagcgtctaaacaggcaatgtttgaaagtgttg	1124	Qy
1096	TGTCTGCTGCTGCAGCCGGCTCGGTTATTGCTTCACCGATTGCCTTATTAGTATCTGGGA	1037	Db
1123	ttccgctgctgctgtaggatctgctgttggtgcaccgattgcactattagttgcaggtg	1064	γ
1036	ACTATTGATGCATCGGTTACTGCAATTAATACCGCATTGGC	977	В
1063	tactattgaagcttcattaactacaattagtacggcattaggtgcagtttctgctggt	1004	δ
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1003	tccgaaaatttggctatgatggggatcatttattggctgaatatcagcgtggtgt	944	νQ
943 916	catttatgaatgcagcagataaattcaatcatgctaatgctcttgatgagtttgcaaaac	884 857	B 64
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883	ctactggtgctgttgctgctttaattacttcatcgattatgttggcaattagtcctttgg	824	Qy
796	TATCTT	737	В
823	gtaacaaaagcaatttcttcatatgttttagcacaacgtgttgctgctggtctatcaa	764	Q
736		677	рь
763	catcgactggcaaaaagttgctgcaggttttgaattaagcaatcaagttattggta	704	Qy
7	GTTATCTCAGGGCTATTATCGGGCGCAACAGCTGCACTTGTACTTGCAGATAAAA		дь :
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w	CTGGAATGGATTTAGATGAGGCCTTACAGAATAACAGCAACCAACATGCTCTTGCTA		В
σ	cgggtatagaacttgattctttaatcaaaaaaggtgatgctgcacctgatgctttggcta	0	Qy

	gttatatcacttccgatcaaattgataaaatttt 2567 	2534	Qy
2533	ttatcaaagtaataaaacagatcataaaattgagcaactaattggtaaagatggta	2478	Qy
2527		2468	Db
2477 2467	atcattcaggtagtattaacataccaagatggtacataacatcaaatttacaaaa	2423 2408	Оу
2422	caaatatatctgatattatgattgaacgtaccaaagagggtattataggttaaacgaaatg	2363 2351	Оу
2362	ttgtacgatggcacgggcaatgataaattagcatttgcagatg	2303	Qy
2350		2291	Db
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NN	ttggtggtaaaggcaacgatcgacttctggagatgaaggcgatgatttactcgatggcg	2183	Qy
		2171	Db
2182	tattccatagtggtgaaggtgatgatttactcgatggtggtgctggtgacgaccgcttgt	2123	Qy
2170		2111	Db
2122	tagaagaagtaattggttctcaatttaatgatgtattcaaaggttctaaattcaacgaca	2063	Qy
2110		2051	Db
2062	gtgattatgaattaagaaaagttgggtatggttatcagtctaccgataatttgaaatcag	2003	Qy
		1994	dd
2002 1993	cagtatc GAATATC	1943 1934	Qy Db
1942 1933	tcgaggtgatatctacc AACCGGTAAAGCACTAC	1883 1874	Qy Db
1882	acgatcgtgtcttctatagtaaagacggaggatttggtaatattactgtagatggtacga	1823	Оу
1873		1817	
1822	<pre>ctggcaatgacgatatctttgttggtcaaggtaaaatgaatattgatggtggagatggac </pre>	1763	Qy
1816		1757	Db
1762	ABGGCACBGACATGGTAAACTAAAACCAAAGAAACAAAAATTATTGCCAAACTTGGTG	1724	Qy
1756		1697	Db
1723	atggagaggctagttctaaattagatttctctaaagttattcagcgtgtagccgagacag	1664	Qy
1696		1637	
1663	gtaaatactcttatattaataagttaaaattcggacgtgtaaaaaaactggcaagttacag	1604	Qy
1636		1577	Db
1603	tgoatttoacttogcotttgttaacagcaggaactgaatcacgtgaacgtttaactaatg	1544	Qy
1576		1517	Db
1516		1457	Db

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US-08-878-748-5
; Sequence 5, Application US/08878748
; Patent No. 5969126
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; LOCATION:
US-08-878-748-5
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Best Local S
Matches 1538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: GORH-LE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                  FEATURE:
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CITY: PALO ALTO
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nes 1538; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: ROBINS, ROBERTA L. REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 9001-0016.21
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                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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                                                                                                                                    AAAGAGAAGAACGCAATAATATTGCAACAGCTCAAACCAGTTTAGGCACGATTCAAACCG
                                tagcagaagagcctaatcacactgaaacagcaaaaaaatctgttgacacagtaaatcagt
                                                                                        aaaaaggtgggactttaaaatgattttattaaagctgctgatgaattaggtattgctcgtt 166
                                                                                                                                                              caaagtctggattaaaaaatctttacttggctattcccaaagat-----tatgatccgc 106
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                                                                          AACAAGGTAATGGTTTACAGGATTTAGTCAAAGCGGCCGAAGAGTTGGGGATTGAGGTAC
                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                         2794 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                    (415) 617-8999
(415) 327-3231
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Pred. No. 2.9e-
0; Mismatches
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                                                                                                                   Query Match
Best Local Similarity
Matches 1538; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 327-32 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                        NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 901
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L. ROBINS
STREET: 285 HAMILTON AVENUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HARLAND, RICHARD J.
TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER
TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED
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APPLICANT:
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                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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CITY: PALO ALTO
STATE: CALIFORNIA
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                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                      TYPE:
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               atcattcaggtagtattaacataccaagatggtacataacatcaaatttacaaaa-----
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AACAAGGTAATGGTTTACAGGATTTAGTCAAAGCGGCCGAAGAGTTGGGGGATTGAGGTAC 148
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                                                                                                                    Conservative
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415) 327-3231
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                                                                                                                 Score 814.4; DB 2;
Pred. No. 2.9e-177;
0; Mismatches 956;
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WITH IRON-REGULATED PROTEINS
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                                                                                                                                             Length 2794;
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1303	ttgataaaggctatgattctcgttatgctgcttatttagctaataacttaaaatttttgt	1244	Qy
1216	AAATAAAATTCATAACAAAATTGTAGAATGGGAAAAAATAATCACGGTAAGAACTAC	1157	Дb
1243	ccgtttacaaggtaaaatt	1184	Qy
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76		917	Db x3
943 916	atttatgaatgcagcagataaattcaatcatgctaatgctcttgagtttgcaaa	884 857	D 09
υ α	$\alpha - \alpha$		Дb
823 796	atgtaacaaaagcaatttcttcatatgttttagcacaacgtgttgctgctggtctatcaa 	764 737	ОУ
763 736	atgcatcgactggcaaaaaagttgctgcaggttttgaattaagcaatcaagttattggta 	704 677	Qy
703 676	tggaaataattactggtttgctatcaggcatttctgcaggctttgctttagcggataaaa	644 617	Qy Db
643 616	tototaatataggaaacaagttgcaaaacottaaatttttotaaaacaaatottggtt	587 557	Дb
586 556	ttgaagcattttcttcacagttagcaaagttaggttctactatatcgcaggctaaaggct	527 497	ОУ
526 496	aagctagtattgacttgattaatgagataattggtaatctatct	467 437	Оу
466 436	cgggtatagaacttgattctttaatcaaaaaaggtgatgctgcacctgatgctttggcta	407 380	Qy Db
406 379	gtaatgtattatcaacattäagctcttttttgggcactgcattag 	347 320	ОУ
346 319	.agccaaaggttagacagtgtagaaaatattgatcgta 	287 269	Оy
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                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION NUMBER: US 07/779,171
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
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                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE,
                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                            REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (4.5)327-3400
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: POTTER, ANDREW A. APPLICANT: MANNS, JOHN G. TITLE OF INVENTION: GNRH-LEU
                                                    MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 34
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CITY: PALO ALTO
STATE: CA
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                                   NAME/KEY:
                                                                                      TOPOLOGY:
                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 94301
                                                                                                       STRANDEDNESS:
                                                                                                                                          LENGTH:
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Best Local Similarity
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                                                     catttatgaatgcagcagataaattcaatcatgctaatgctcttgatgagtttgcaaaac 943
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GGACTATTGATGCATCGGTTACTGCAATTAATACCGCATTGGCCGCTATTGCTGGTGGTG
                                                                                                             CATTTGCCGGTATTGCCGATAAATTTAATCATGCAAAAAGTTTAGAGAGTTATGCCGAAC
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Pred. No. 2.9e
0; Mismatches
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2.9e-177;
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APPLICATION NUMBER: US/08/15
FILING DATE: 09-FBB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 504,850
FILING DATE: 05-APR-1990
APPLICATION NUMBER: 335,018
FILING DATE: 07-APR-1989
SEQ ID NO:2:
LENGTH: 2794
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5476657-2
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APPLICANT: POTTER, ANDREW A.

TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA

COMPOSITIONS AND USES THERROF

NUMBER OF SEQUENCES: 8
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Best Local Similarity 60.2%;
Matches 1538; Conservative
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ctattggcttaactgagcgtggcattgtgttatccgctccacaaattgataaattgctac
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Pred. No. 2.9e
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1336	277 tgaacttaaacaaagagttacaggcagaacgtgtcatcgctattactcagc	Db 1
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466 436	aaaaaaggtgatgctgcacctgatgctttggcta 	Qy
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; LOCATION:
US-07-960-932-9
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US-07-960-932-9
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Best Local
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2817 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: POTTER, A
APPLICANT: REDMOND,
APPLICANT: HUGHES, H
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 901
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19921014
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
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                                                                                                                                                                                  GTAAAGGCAACGACCTATTACACGGTGGCAAGGGCGATGATATTTTCGTTCACCGTAAAG
                                                                                                                                                                                                                                                                                                                       ttggtggtaaaggcaacgatcgactttctggagatgaatgcgatgatttactcgatggcg 2242
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                                                          Query Match
Best Local Similarity
Matches 1538; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                    TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2817 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: ENHANCE
TITLE OF INVENTION: CHIMERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2468
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                                                                                                                                                                             FEATURE:
                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                   NAME/KEY:
LOCATION:
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CITY: PALO ALTO
STATE: CALIFORNIA
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                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                        STRANDEDNESS: double
                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                          NAME: ROBINS, ROBERTA
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0' FILING DATE: 14-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/01 FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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AGCGGATCACCTCAAAGCAAGTTGATGATCTTAT
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                                                          Conservative
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327-3231
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                                                          Score 814.4; DB 1;
Pred. No. 2.9e-177;
0; Mismatches 956;
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1063	04 gtactattgaagcttcattaactacaattagtacggcattaggtgcagtttctgctggtg	
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466 436	7 cgggtätagaacttgattetttaateaaaaaaggtgatgetgeacetgatgetttggeta	
406 379	7 aattaggtaaagcaagtaatgtattatcaacattaagctcttttttgggcactgcattag	Db
346 319	187 aaaaacattctaccaataagttagccaaagggttagacagtgtagaaaatattgatcgta 	Дb
286 268	27 ttctctctctcacacaaactggtattgctatt	ОУ
226 208	49	Qy Db
166 148	107 aaaaaggtgggactttaaatgattttattaaagctgctgatgaattaggtattgctcgtt 	Оу

Qy	Db	Qy	Db 92		Дb	Дb	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Дb	VQ	Db	Qγ	מם	γQ	дb	Qy	Db	QV	Db	04	Db.	Oy	Дb	γQ	da ga	۰ ٥٧	da da	0
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gttctggtgatgatgtattaaatggtggtgctggtaatgatgtctatatctttcggaaag 23	TGGTGGAAATGGTGATGATTTTATCGATGGCG 22	tggtggtaaaggcaacgatcgactttctggagatgaaggcgatgatttactcgatggcg 22	calculated by by leading the calculation of the c	attoostaataataataataataataataataataataataataa	ט נ	TCATAGCAATAACCAGCACCATGCCGGTTATTACACCAAAGATACCTTGAAAGCT	aagttgggtatggttatcagtctaccgataatttgaaatcag 20	GACTTCAACCCAT	gaagttgtgaagcgtcaagaaaccaaggtgggtaaacgtactgaaactatccagtatc 20	AAGGTAGTTATACCGTAAATCGTTTCGTAGAAACCGGTA	caacagaagcaggcagttatacagttaatcgtaaggttgctcgaggtgatatcta	CCGTGGAAACTATGGTGCTTTAACTATTGATGCAACCA 1	gatcgtgtcttctatagtaaagacggaggatttggtaatattactgtagatggtacg	ACGGAAATTGATGGCGGTGAAGGTT 1	gcaatgacgatatctttgttggtcaaggtaaaatgaatattgatggtggagatggac l		gcacagacgagattggtctaatagtaaatgcaaaa		gagaggetagitetaaattagaittetetaaaqitaiteaqeqiqtaqeeqaqaeaq l	GAATATTACCAAGCTCAATATTAACCGTGTAGATAGCTGGAAAATTACAG 1	cottatattaataagitaaaattoggacgigtaaaaaaciggcaagitacag 1	ACGCCGGGAACAGAGCATCGTGAACGCGTACAAACAG 1	acttegeetttgttaacaqeaqqaactqaateaeqtqaacqtttaactaatq 1	GCADACGGTATTATTGATGTGAGTAATTCGGGTAAAGCGAAAACTCAGCATA 1	######################################	- }-∺	T TIDDITOLITACIONALIMATERIA CONTINUE CO	ATAACAACATTGGTGATTTAGCTGGTATTTAGCTGTTTAGGTGAAAAAGTTCTTTAGTGGTA 13	ataatattqqtqaqttaqcaqqtattaccaaattqqqtqaacqcattaaqqqqqaa 1	GAACTTAAACAAAGAGTTACAGGCAGAACGTCTCATCGCTATTACTTAGCAGCAGCAATGGC 1	agctaaataaagagttggaagctgaacgtgttattgcaatcacccaacaacgttggg l		######################################	CAAATAAAATTCATAACAAAATTGTAGGAAAAAAAAATAATCAGGGTAAGAACTACT 1	Ctaaccutttacaaqqtaaaattttaqaqtqqqaaaaqqqaaatqqqqqqqq
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM_PC_COMPATIBLE
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PATENTIAN
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/960,932
FILING DATE: 19921014
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2838 base pairs
                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
RECISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: REDMOND, MARK J. APPLICANT: HUGHES, HUW P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2528 AGCGGATCACCTCAAAGCAAGTTGATGATCTTAT
                                                                                                                                 MOLECULE TYPE:
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CITY: PALO ALTO
STATE: CALIFORN
                                                                                                                                                  TOPOLOGY:
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                                                                                                  NAME/KEY:
                                                                                                                                                              STRANDEDNESS:
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635 BRYANT
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                                                                                                  CDS
                                                                                                                                                  linear
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MBXA.

Moraxella bovis.
Bacteria; Proteobacteria;
NCBI_TaxID=476;
[1]

gamma subdivision; Moraxellaceae; Moraxella.

093GI2; 093GI2; 01-DEC-2001 01-DEC-2001 01-DEC-2001 RTX TOXIN.

(TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 19,

Created)
Last sequence update)
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PRELIMINARY;

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Q937v7 bordetella		Q937v4 bordetella	Q937v5 bordetella	7v9		Q937wl bordetella	Q937w0 bordetella	Q9jtu8 neisseria m	Q937v6 bordetella	Q51868 pasteurella	3 xylella	xylella f	w	Q51865 pasteurella	Q91469 bordetella				Q46716 escherichia	P71223 escherichia				Q93npO actinobacil	Q9rcg8 pasteurella	•		Q9ev22 pasteurella

ALIGNMENTS

ytotoxin gene."; 4; 4; agth 927; dels 0; Gaps abeLGIARLAEEP 60 abeLGIARLAEEP 60 bSVENIDRKLGKA 120 bSVENIDRKLGKA 120	OY 121 SNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFS 180	Qy 61 NHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKA	Qy 1 MSNINVIKSNIQAGLNSTKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEP 60	Query Match 100.0%; Score 4646; DB 2; Length 927; Best Local Similarity 100.0%; Pred. No. 7.8e-199; Matches 927; Conservative 0; Mismatches 0; Indels C	SQ SEQUENCE 927 AA; 98845 MW; F4B703577E10A96D CRC64;	DR EMBL; AF205359; AAK84651.1;	RL Am. J. Vet. Res. 62:1222-1228(2001).	RA Angelos J.A., Hess J.F., George L.W.;	RX MEDLINE=21388402; PubMed=11497442;	RC STRAIN-TIFTON I;	RP SEQUENCE FROM N.A.
	EIIGNLSQSTQTIEAFS 180	AKGLDSVENIDRKLGKA 120 	FIKAADELGIARLAEEP 60 	Length 927 Indels	CRC64;			is cytotoxin gene.":			

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Q9EV24;
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                                                                                                                                           Bacteria; Proteobacteria; Mannheimia.
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 MEDITINE-21101823; PubMed-11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of
Gene in Bovine and Ovine Strains of Mannheimia
                                                                     SEQUENCE FROM N.A. STRAIN=PH574;
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REMBL; AF314521; AAG40305.1; -.

InterPro; IPR001753; Enoyl_Co_hydrtse.

InterPro; IPR001343; Hemlysn_Ca_bind.

InterPro; IPR003355; RTX_N.

Pfam; PF00353; hemolysinCabind; 1.

Pfam; PF02382; RTX; 1.

PFANTS; PR00313; CABNDWGRPT.

PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.

PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
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                                                           RGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKG
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        IVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVA
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                                                                                                                                 ERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRV----
SKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDV
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 49.9%; Pi 71; Conservative 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                           50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2358.5;
Pred. No. 4.1e
82; Mismatches
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4.1e-97;
nes 258;
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Best Local Similarity
Matches 471; Conserv
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Q9EV23;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol. 183:1394-1404(2001).
EMBL; AF314522; AAG40306.1; -.
InterPro; IPR001753; Encyl_Coa_hyd
InterPro; IPR001343; Hemlysn_Ca_bi
InterPro; IPR003355; RTX_N.
                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00353; hemolysinGabind; 1.
Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1
SEQUENCE 953 AA; 102150 MW; D99C36DA595B1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davies R.L., Whittam T.S., Selander R.K.; "Sequence Diversity and Molecular Evolution of Gene in Bovine and Ovine Strains of Mannheimia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Davies R.L., Whittam T.S., Selande "Sequence Diversity and Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21101823; PubMed-11157953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mannheimia glucosida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  haemolytica.";
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ITSSIMLAISPLAFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLT
                                                                                   SLIENIANSVKTLDAFGDQINQLGSKLQNVKGLSSLGDKLKGLSGFDKTSLGLDVVSGLL
                                                                                                                                        EIIGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNLN-FSKTNLGLEIITGLL :| |:: | :| |: | | |:::||
                                                                                                                                                                                           AKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLIN
                                                                                                                                                                                                                             LLKHS~KNVTNSLDKLISSASAFTSSNDSRNVLVAPTSMLDQSL
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                                                                                                                                                                        GQAIGSAENLTKGFSNAKTVLSGIQSILGSVLAGMDLDEALQK-NSNELTLAKAGLELTN
                                                                                                                                                                                                                  LVKAAEELGIEVQKEEGNDIAKAQTSLGTIQNVLGLTERGIVLSAPQLDKLLQK---TKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFAKEVRNYKATK-DEKIEEIIGQNGERITSKQVDDLI--AKGNGKITQDELSKVVDNYE
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RTX_N.
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Last sequence update)
Last annotation updat
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Pred. No. 5
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5.4e-97;
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Q9ETX2;
01-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                                                                         "Sequence diversity and molecular evolution of gene in bovine and ovine strains of Mannheimia haemolytica.";
                                        InterPro; IPR003355; RTX_N.

Pfam; PF00353; hemolysinCabind; 1.

Pfam; PF00382; RTX; 1.

PRINTS; PR00313; CABMUNGRPT

PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.

SEQUENCE 953 AA; 102135 MW; 70DB354157F5881E
                                                                                                     EMBL; AF314518; AAG40302.1; -.
EMBL; AF314517; AAG40301.1; -.
InterPro; IPR001753; Enoyl_CoA_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
                                                                                                                                                                                          STRAIN=PH498, AND PH344;
Davies R.L., Whittam T.S
                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                       NCBI_TaxID=85401;
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16,
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Last sequence up
Last annotation
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No. 6e-97;
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                                            CRC64;
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Query Match Best Local Similarity

50 49 .7%;

Score Pred.

Length

Matches

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CT.

181

164 122 104 65 44

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Q9EV25;
Q9EV25;
01-MAR-2001
01-MAR-2001
                                                                                                   KVVDNYELLKHS-KNVTNSLDKLISSASAFTSSNDSRNVLVAPTSMLDQSL
                                                                                                                                                 KLADENKSQKLSASDIASSLNKLVGSMALFGTANSVSSNALQPITQPTQGI
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      (TrEMBLrel.
                                        PRELIMINARY;
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Best Local Similarity
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EMBL; AF314520; AAG40304.1; -.
InterPro; IPR001753; Enoyl_Coa_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
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PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.

SEQUENCE 953 AA; 102138 MW; C41D9EBC1D799951 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21101823; PubMed=11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of Gene in Bovine and Ovine Strains of Mannheimia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00353; hemolysinCabind; Pfam; PF02382; RTX; 1.
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NCBI_TaxID=85401;
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Bacteria; Proteobacteria;
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                                                                                                                                                LEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELA 462
GTDEIGLIVNAKAGNDDIFYGQGKMNIDGGDGHDRVFYSKDGGFGNITYDGTSATEAGSY
                                                   TAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVTQRV-----AETE
                                                                                                 GITKLGERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLL
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                                      TPGTEHRERVQTGKYEYITKLNINRVDSWKITDGAASSTFDLTNVVQRIGIELDNAGNVT
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49.5%;
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Pred. No. 6e-97;
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Best Local Similarity
Matches 468; Conserv
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Q9EV26;
Q1-MAR-2001
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                       Pfam; PF00353; hemolysinCabind; Pfam; PF02382; RTX; 1. PRINTS; PR00313; CABNDUGRPT. PROSITS; PS00166; ENOYL_COA_HYDE SEQUENCE 953 AA; 102236 MW;
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF314519; AAG40303.1; InterPro; IPR001343; Hemlysn_Ca_bind. InterPro; IPR001343; Hemlysn_Ca_bind. InterPro; IPR003355; RTX_N.
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Bacteria; Proteobacteria;
Mannheimia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol.
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                                                      AKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLIN
                                                                                                  LVKAAEELGIEVQKEEGNDIAKAQTSLGTIQNVLGLTERGIVLSAPQLDKLLQK---TKV
                                                                                                                    KLADENKSQKLSASDIASSLNKLYGSMALFGTANSVSSNALQPITQPTQGI
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Q9EV32;
Q1-MAR-2001
01-MAR-2001
01-DEC-2001
              MEDLINE=21101823; PubMed=11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution
Gene in Bovine and Ovine Strains of Mannheim
                                                                                                                                                   Pasteurella haemolytica.
Bacteria; Proteobacteria;
Mannheimia.
                                                                                    STRAIN-PH706;
                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                     NCBI_TaxID=75985;
                                                                                                                                                                                                        LKTA.
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                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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19,
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Last sequence update)
Last annotation update)
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volution of Mannheimia

the Leukotoxin (Pasteurella)

Pasteurellaceae;

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PRWY----ITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQ------DKKD-GTV
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VDNYELLK-----HSKNVTNSLDKLISSASAFTSSNDSRNVLVAPTSMLDQSL
                                              ITSQELKKLADENKSQKLSASDIASSLNKLVGSMALFGTANSVSSNALQPITQPTQGI 922
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InterPro; IPR001753; Enoyl_CoA_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR001345; RTX_N.
Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNUNGRPT.
PROSITE; PR000166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 953 AA; 102078 MW; EF425243C8741EE4
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 PRWY----ITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELK
                                           GGAGNDVYIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINI
                                                                    PNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLN
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                      TVNRFVESGKALHEVTSTHTALVGNREEKIEYR-HSNNQHHAGYYTKDTLKAVEEIIGTS
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InterPro; IPR001753; Enoyl_CoA_hydrtse.

InterPro; IPR001343; Hemlysn_Ca_bind.

InterPro; IPR003355; RTX_N.

Pfam; PF00353; hemolysinCabind; 1.

Pfam; PF00382; RTX; 1.

PFANT; PF00382; RTX; 1.

PRINTS; PR00313; CABNUNGRPT.

PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.

SEQUENCE 953 AA; 102132 MW; 4138AB5FAE2843B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21101823; PubMed=11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of
Gene in Bovine and Ovine Strains of Mannheimia
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AINTALAAIAGGVSAAAAGSVVASPIALLVSGITGVISTILQYSKQAMFEHVANKIHNKI
           TISTALGAVSAGVSAAAVGSAVGAPIALLVAGVTGLISGILEASKQAMFESVANRLQGKI
                                           SGATAALVLADKNASTSRKVGAGFELANQVVGNITKAVSSYILAQRVAAGLSSTGPVAAL
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Pred. No. 4e-96;
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Davies R.L., Campbell S., Whittam T.S.;

"Mosaic structure and molecular evolution of the leuk
(lktCABD) of Mannheimia (pasteurella) haemolytica, Ma

"glucosida and Pasteurella trehalosi.";

J. Bacteriol. 0:0-0(2001).

R EMBL; AF314515; AAG40299.1; -

R EMBL; AF41411; AAL13281.1; -

R InterPro; IPR001343; HemlySn_Ca_bind.

R InterPro; IPR001343; HemlySn_Ca_bind.

R InterPro; IPR001343; HemlySn_Ca_bind.

R Ffam; PF00353; hemolysinCabind; 1.
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SEQUENCE FROM N.A.
STRAIN-PH292, AND PH296;
STRAIN-PH292, AND PH296;
MEDLINE-21101823; PubMed-11157953;
MEDLINE-21101823; PubMed-11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution"
"Sequence Diversity and Molecular Evolution and Molecular Evolution of Mannheim"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Mannheimia.
                                                                                                                                                                                                                                                                                  STRAIN-PH296;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Best Local S
Matches 474
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PRINTS; PR00313; CABNDNGRPT.
PROSTTE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 953 AA; 102218 MW; 04AB1715B619E571
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                    QNWFREAEFAKTIQNYVATR-DDKIEEIIGQNGERITSKQVDELIE--KGNGKIAQSELT
                                                                                           TVNREVESGKALHEVTSTHTALVGNREEKIEYR-HSNNQHHAGYYTKDTLKAVEEIIGTS
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Pred. No. 6e-96;
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Best Local Similarity 50.1
Conservative
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EMBL; AF314504; AAG40288.1; -.
EMBL; AF314504; AAG40288.1; -.
EMBL; AF314506; AAG40290.1; -.
InterPro; IPR001753; Emoyl_CoA_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR00335; RTX_N.
Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF00313; CABNDNGRPT.
PROSITE; PR00313; CABNDNGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UN
SEQUENCE 953 AA; 101997 MW; D593D6A57
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Q9ETG5;
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STRAIN-PH284, PH388, AND PH8;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence diversity and molecular evolution of
gene in bovine and ovine strains of Mannheimia
haemolytica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pasteurella haemolytica.
Bacteria; Proteobacteria;
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ASPIALLVSGITGVISTILQYSKQAMFEHVANKIHNKIVEWEKNNHGKNYFENGYDARYL
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KKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLK
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D593D6A577C3ADE9
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.3e-96;
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RESULT 11
Q9EV31
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                                                                                                      Query Match
Best Local Similarity
Matches 469; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pasteurellà haemolytica.
Bacteria; Proteobacteria;
Mannheimia.
                                                                                                                                                                                                                                                                  Pfam; PF00353; hemolysinCabind; Pfam; PF02382; RTX; 1. RTX; PRINTS; PRO0313; CABNUNGRPT. PROSITE; PS00166; ENOYL_COA_HYDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21101823; pubMed=11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of
Gene in Bovine and Ovine Strains of Mannheimia
                                                                                                                                                                                                                                                                                                                                                                                                                                     haemolytica.";
J. Bacteriol. 183:1394-1404(2001).
EMBL; AF314510; AAG44294.1; -.
InterPro; IPR001753; Enoyl_CoA_hydrtse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=PH588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
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NAGQSLAKAG-QSLKTGAKKIILYIPKDYQYDTEKGNGLQDLVKAAQELGIEVQKEEGND
                                                NVIKSNIQAGLNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNH
                                                                                                                                                                                                                                            PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
953 AA; 102160 MW; A189BF80754A7907 CRC64;
                                                                                                            Conservative
                                                                                                      50.1%; So
50.1%; Pr
tive 178;
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Last sequence up
                                                                                                      Score 2329.5; DB 2
Pred. No. 8.1e-96;
8; Mismatches 259;
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Q9EV27;
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01-MAR-2001
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LEUKOTOXIN.
  Pasteurella haemolytica.
Bacteria; Proteobacteria;
Mannheimia.
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                    subdivision;
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Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNUNGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 953 AA; 102230 MW; 2B686808EB370090
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InterPro; IPR001753; Enoyl_(
InterPro; IPR001343; Hemlysi
InterPro; IPR003355; RTX_N.
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TVNREVESGKALHEVTSTHTALVGNREEKIEYR-HSNNQHHAGYYTKDTLKAVEEIIGTS
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Pred. No. 8.1e-96;
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Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of Gene in Bovine and Ovine Strains of Mannheimia haemolytica.";
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Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 953 AA; 102147 MW; 11600FDA7849A1CA
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EMBL; AF314514; AAG40298.1; -
InterPro; IPR001753; Encyl_Coa_hydrtse
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
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VGAGFELANQVVGNITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIAD
                                                                                                                                                                                         VLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQ
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01-DEC-2001
LEUKOTOXIN.
                                                                                                                                                                              Pasteurella haemolytica.
Bacteria; Proteobacteria;
Mannheimia.
                                                                                 MEDLINE=21101823; PubMed=11157953; Davies R.L., Whittam T.S., Selander R.K.; Davies R. Diversity and Molecular Evolution Gene in Bovine and Ovine Strains of Mannheir
           EMBL; AF314505; AAG40289.1; InterPro; IPR001753; Enoyl CoA_hydrtse. InterPro; IPR001434; Hemlysn_Ca_bind. InterPro; IPR003355; RTX_N.
                                                                                                                                                                                                                                                                Q9EV34;
01-MAR-2001
                                                                                                                                                                                                                                                                                        Q9EV34
                                                           J. Bacteriol.
                                                                                                                                  STRAIN-PH56;
                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                  NCBI_TaxID=75985;
                                                                     haemolytica.";
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KLNINRVDSWKITDGAASSTFDLTNVVQRIGIELDNAGNVTKTKETKIIAKLGEGDDNVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGSGTTEIDGGEGYDRVHYSR-GNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEGKHIKADKLVQLDSANGIIDVSNSGKAKTQHILFRTPLLTPGTEHRERVQTGKYEYIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KFNHAKSLESYAERFKKLGYDGDNLLAEYQRGTGTTDASVTAINTALAAIAGGVSAAAAG
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                                                                               in Bovine and
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  PF00353;
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L (TrEMBLrel.
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                                                           183:1394-1404(2001).
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16,
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Last sequence
Last annotation
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annotation
                                                                                   Volution of Mannheimia
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                                                                                                the Leukotoxin
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Best Local S
Matches 464
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PRINTS; PR00313; CABNDNGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
DE48B28EE0EB09FB CRC64;
                                                                                                                                                                                         598
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ASPIALLVSGITGVISTILQYSKQAMFEHVANKIHNKIVEWEKNNHGKNYFENGYDARYL
                                                                                                                                                                                                        LISSVSAFTSSNDSRNVLVAPTSMLDQSL
               LVGSMALFGTANSVSSNALQPITQPTQGI
                                          HKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNK
                                                                           TGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTD
                                                                                                  VGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDL
                                                                                                                                                                                 GKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETK
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                                                                                                                                                                                                                                                                                                                                                                                                                   KSNIQAGLNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTET
                                 EKIEETIGQNGERITSKQVDDLI--AKGNGKITQDELSKVVDNYELLKHS-KNVTNSLDK
                                                                  DGNDKLSFSDSNLKDLTFEKVKHNLVI-TNSKKEKVTIQDWFREADFAKEVPNYKATK-D
                                                                                                                                     VGNREEKIEYR-HSNNOHHAGYYTKDTLKAVEEIIGTSHNDIFKGSKFNDAFNGGDGVDT
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464; Conserv
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Pred. No. 1.2e-
75; Mismatches
                 922
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1.2e-95;
nes 264;
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Best Local S
Matches 463
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J. Bacteriol. 0:0-0(2001).

EMBL; AF314513; AAG40297.1; -.

EMBL; AF314511; AAG40295.1; -.

Interpro; IPR001753; Enoyl_CoA_hydrtse.

Interpro; IPR001343; Hemlysn_Ca_bind.

Interpro; IPR003355; RTX_N.

Pfam; PF00353; hemolysinCabind; 1.

pfam; PF00353; CABLNDGRPT.

PROSITE; PR003166; ENOYL_COA_HYDRATASE; UN
SEQUENCE 954 AA; 102410 MW; 02A60E524
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SEQUENCE FROM N.A.
STRAIN=PH202, AND PH494;
Davies R.L., Whittam T.S., Selander R.K.;
Davies R.L., and molecular evolution of
"Sequence diversity and molecular evolution of
hovine and ovine strains of Mannheimia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9EUE1;
Q9EUE1;
01-MAR-2001
01-MAR-2001
01-JUN-2001
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Bacteria; Proteobacteria;
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                        482
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                                                             LAKLGSTISQAKGFSNIGNKLQNLN-FSKTNLGLEIITGLLSGISAGFALADKNASTGKK
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l (TrEMBLrel. 16,
l (TrEMBLrel. 17,
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Last seg
Last ann
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Pred. No. 2.2e-95;
7; Mismatches 248;
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02A60E52411711A2
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annotation updat
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Db	500	EEGKHLKADKLVQLDSANGIIDVSNSGKAKTQHILFRTPLLTPGTEKRERVQTGKYEYIT 559	9
Qy	542	KLKFGRVKNWQVTDGEASSKLDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIF 594	94
Db	560	560 KLNINRVDSWKITDGEASSTEDLTNVVQRIGIELDNAGNVTKTKETKIIAKLGEGDDNVF 619	19
Qy	595	VGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQ 654	54
Db	620	VGSGTTEIDGGEGYDRVHYSR-GNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTH 678	78
Qy	655	ETKVGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEG 714	14
DЬ	679	TALVGSREEKIEYRHSNNRQHA-GYYTKDTLTSIEEIIGTSHNDIFKGSQFNDAFNGGDG 7	737
Qy	715	DDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTL 774	74
Db	738	738 VDTIDGNGCNDRLFGGKGDDIIDGGDGDDFIDGGKGNDLLHGGRGDDIFVHRQGDGNDSI 7	797
Qy	775	YDGTGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWYITSNLQNYQSN 830	30
рь	798	TEAGGHDRLSFSDSNLKDLTFEKVNHHLVI-TNTKQEKVTIQNWFREEEFAKTVKNYVAT 8	856
Qy	831	KTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKL 882	82
Db	857	Χ	905
VΩ	883	SASDIASSLNKLYGSMALFGTANSVSSNAL 912	
DЪ	906	NSRNVINSLDKLISSVSSFTSSND-SRNVL 934	

Search completed: September 11, 2002, 09:01:25 Job time: 283 sec

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ALIGNMENTS

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; MOLECULE TYPE: protein US-07-777-715-7
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US-07-777-715-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application Patent No. 5273889 GENERAL INFORMATION:
                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Robins, Roberta L.
NAME: Robins, Roberta J. 208
                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                 REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 29;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Potter, Andrew APPLICANT: Campos, Manuel APPLICANT: Hughes, Huw P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: CYTOKINE-LEUKOTOXIN GENE FUSIONS AND TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                      TELEPHONE: 415-327-72
TELEFAX: 415-327-2951
TELEX: 706141
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 199110 CLASSIFICATION: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Morrison & Foerster STREET: 545 Middlefield Road, 9 CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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8 KSNIQAGLNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTET

Matches 465;

Conservative 175;

50.2%; Score 2334; DB 1; 50.1%; Pred. No. 8.8e-175; tive 175; Mismatches 263;

Length 1098; Indels 26;

13;

Best Local Similarity

Query Match

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                                                                                  US-08-170-126-2
                                                            Sequence 2, Application Patent No. 5594107
                                                     GENERAL INFORMATION:
APPLICANT: POTTER, APPLICANT: CAMPOS, I APPLICANT: HOMERS, I APPLICANT: HOMERS, I TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173
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                                                                                                                                                                EKIEEIIGQNGERITSKQVDDLI--AKGNGKITQDELSKVVDNYELLKHS-KNVTNSLDK
                                                                                                                                                                                  HKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNK 893
                                                                                                                                                                                                          DGNDKLSFSDSNLKDLTFEKVKHNLVI-TNSKKEKVTIQNWFREADFAKEVPNYKATK-D
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                                                                                                                                             LVGSMALFGTANSVSSNALQPITQPTQGI
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APPLICATION NUMBER: US 07/571
APPLICATION NUMBER: US 07/571
ATTORNEY/ACENT INFORMATION:

NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-899
TELEPAX: (415) 627-3231
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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APPLICATION NUMBER: US 07/777,715
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STREET: 635 BRYANT
CITY: PALO ALTO
STATE: CALIFORNIA
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                                                                                                                                                GFELSNOVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFN
ANLQDNMKFLLNLNKELQAERVIAITQQQWDNNIGDLAGISRLGEKVLSGKAYVDAFEEG
                                                                                            GAPIAILVAGVTGLISGILEASKQAMPESVANRLQGKILEMEKQNGGQNYFDKGYDSRYA 424
                                                                                                                                                                                                                        GFELANQVVGNITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFN
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                                                                             ASPIALLVSGITGVISTILQYSKQAMFEHVANKIHNKIVEWEKNNHGKNYFENGYDARYL
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RESULT 3
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TELEFAX: (415) 327-3231 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/17(
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
ATTORNEY/AGENT INFORMATION:
ANDEE: CERETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                 REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 900
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: REED & RC
                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
ZIP: 94301
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STATE: CALIFORNIA
                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                   NAME: ROBINS, ROBERTA L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              635 BRYANT
                                                                                                                                                                                                                                                                                                                                                                                                UNITED STATES
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; LENGTH: 1098 amino a
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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LVGSMALFGTANSVSSNALQPITQPTQGI
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                                                                                                DGNDKLSFSDSNLKDLTFEKVKHNLVI-TNSKKEKVTIQNWFREADFAKEVPNYKATK-D
                                                                                                                         TGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTD
                                                                                                                                                                                                                          VGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDL
                                                                                                                                                                                                                                                                                 GKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETK
                                                                                                                                                                                                                                                                                                                          INRVDSWKITDGAASSTFDLTNVVQRIGIELDNAGNVTKTKETKIIAKLGEGDDNVFVGS
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                                                                                                                                                                                                                                                                                                                                                                               KHIKADKLVQLDSANGIIDVSNSGKAKTQHILFRTPLLTPGTEHRERVQTGKYEYITKLN
                                                                                                                                                                                                                                                                                                                                                                                               KKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLK 544
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                                         EKIEEIIGQNGERITSKQVDDLI--AKGNGKITQDELSKVVDNYELLKHS-KNVTNSLDK
                                                                     HKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNK 893
                                                                                                                                                                                                                                                                   GTTEIDGGEGYDRVHYSR-GNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTAL
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465; Conserv
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               922
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Patent No. 6100066
                                                                                                                                                                                                                                                                                                                                        Best Local Similarity Matches 461; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 3,208
REFERENCE/DOCKET NUMBER: 900
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: POTTER, ANDREW A.
APPLICANT: THEISEN, MICHAEL
APPLICANT: HARLAND, RICHARD J.
APPLICANT: RIOUX, CLEMENT R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/038,719
FILING DATE: 29-MAR-1993
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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LENGTH: 924 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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STREET: 6:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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                                                                                                                                                                                                      67
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VVGNITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSLES
                         VIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALDE
                                                                IKGLGTLGDKLKNIGGLDKAGLGLDVISGLLSGATAALVLADKNASTAKKVGAGFELANO
                                                                                   AKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQ
                                                                                                                                     SVLAGMDLDEAL-QNNSNQHALAKAGLELTNSLIENIANSVKTLDEFGEQISQFGSKLQN 182
                                                                                                                                                         TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ 192
                                                                                                                                                                                                  IQTAIGLTERGIVLSAPQIDKLLQK---TKAGQALGSAESIVQNANKAKTVLSGIQSILG
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15-MAR-1996
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US-07-908-253-2
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                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
         APPLICATION NUMBER: US/07/908,253 FILING DATE: 19920702 CLASSIFICATION: 420 ATTORNEY/AGENT INFORMATION:
                                                                        SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CITY: PALO ALTO
                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                             ADDRESSEE:
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ROBINS, ROBERTA L
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635 BRYANT
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HAEMOPHILUS SOMNUS OUTER MEMBRANE
PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
                                                                                                                                                                                                                                A L. ROBINS
STREET
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
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TELEPHONE: (415) 617-8999
                                                                                                       781
                                                                                                                                                                                                                543 KITDGAASSTFDLTNVVQRIGIELDNAGNVTKTKETKIIAKLGEGDDNVFVGSGTTEIDG
                                                                                                                                                                                                                                          552 QVTDGEASSKLDFSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG
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REFERENCE/DOCKET NUMBER: 9000-0026
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FSDSNLKDLTFEKVKHNLVI-TNSKKEKVTIQNWFREADFAKEVPNYKATK-DEKIEEII
                   FADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTDHKIEQLI
                                                   DRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLA
                                                                                                                                                             GEGYDRVHYSR-GNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTALVGNREEK
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Pred. No. 2.66
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US-08-455-970A-2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 327-32 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
EILING DATE: 14-OCT-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIAN Release #1.0, V CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,970A
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CITY: CALIFORNIA
CTATE: CALIFORNIA
CTATED ST
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MEDIUM TYPE: Floppy disk
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APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING
TITLE OF INVENTION: CHIMERAS
                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 327-3400
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 90
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                                                         TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ 192
                                                                                                                                                  GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL
AKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQ 251
                            SVLAGMDLDEAL-QNNSNQHALAKAGLELTNSLTENIANSVKTLDEFGEQISQFGSKLQN 182
                                                                                                         FGTANSVSSNALQPITQPTQGI 922
                                                                                       IQTAIGLTERGIVLSAPQIDKLLQK---TKAGQALGSAESIVQNANKAKTVLSGIQSILG
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SYSTEM: PC-DOS/MS-DOS
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174; Mismatches 262;
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APPLICANT: POTTER
                                                                                                                              APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: GRRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                            STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVQLDSANGIIDVSNSGKAKTQHILFRTPLLTPGTEHRERVQTGKYEYITKLNINRVDSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IEYR-HSNNQHHAGYYTKDTLKAVEEIIGTSHNDIFKGSKFNDAFNGGDGVDTIDGNDGN
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                                                                                                                                                                                                                                                                                                             FTSSNDSRNVLVAPTSMLDQSL 917
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-387-156-6
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Best Local (
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
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APPLICATION NUMBER: 10 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNSTKSGLKNLYLAIPKD--YDDQKGGTINDFIKAADELGIARLAEEPNHTETAKKSVDT
                                                                                                                                                                                                                                      SYLAGMDLDEAL-QNNSNQHALAKAGLELTNSLIENIANSYKTLDEFGEQISQFGSKLQN 182
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                                                                                   FAKQERKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAVGAPIALL
GDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTET 664
                                                           QVTDGEASSKLDFSKVIQRV----
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                                     KITDGAASSTFDLTNVVQRIGIELDNAGNVTKTKETKIIAKLGEGDDNVFVGSGTTEIDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: POTTER, ANDREW APPLICANT: MANNS, JOHN G. APPLICANT: MANNS, JOHN G. TITLE OF INVESTIGATION: GDRH-
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CITY: PALO ALTO
STATE: CA
                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 90
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     VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132
                                                      LNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT
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                             LSFPKTGAKKIILYIPQNYQYDTEQGNGLQDLVKAAEELGIEVQREERNNIATAQTSLGT
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                                                                                                                                                                                                                                        (415)327-3231
                                                                              50.1%; Score 2326.5; ilarity 50.0%; Pred. No. 2.60 Conservative 174; Mismatches
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09-AUG-1996
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                                                                                             5; DB 2;
2.6e-174;
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GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: GRRH-LEUK
TOMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
                                                                                                                                                                                                                                                                                                      B
                                                                                                                    Sequence 6, Application US/08878748 Patent No. 5969126
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FGTANSVSSNALQPITQPTQGI 922
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FTSSNDSRNVLVAPTSMLDQSL
                                                                                           GQNGERITSKQVDDLI---AKGNGKITQDELSKVVDNYELLKHS-KNVTNSLDKLISSVSA
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: ROBINS, ROBERTA L
REGISTATION NUMBER: 33,208
REFERENCE, DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 16-OCT-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 14-OCT-1992

PRIOR APPLICATION UNBER: US 07/779,171

FILING DATE: 16-OCT-1991
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423
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CLASSIFICATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                    VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132 : || : || :| :| || || :| ||
                   KFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGS
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MOLECULE TYPE:
US-08-535-837-2
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                                                                                                       TELEFAX: (415) 327-32 INFORMATION FOR SEQ ID NO:
                                                                                                                                     NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 3,208
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
                                                                                                                                                                                                                   FILING DATE: 27-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION UNBER: US/08/535,83; FILING DATE: 27-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                    926 amino acids
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HARLAND, RICHARD J.
VENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE
VENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                   UNITED STATES OF AMERICA
                                     linear
                  protein
                                                                                                                         327-3231
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                                                                                                                                                                                                                                                                                                                 Version
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                                                                                          FGTANSVSSNALQPITQPTQGI 922
                                                                                                                                 GQNGERITSKQVDDLI--AKGNGKITQDELSKVVDNYELLKHS-KNVTNSLDKLISSVSA
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50.0%; Pred. No. 2.60
tive 174; Mismatches
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2.6e-174;
hes 262;
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                                                                                                                                                                                                                                                                                                                                                          Query Match 50.1%; Score 2326.5; DB 3; Best Local Similarity 50.0%; Pred. No. 2.6e-174; Matches 461; Conservative 174; Mismatches 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
TELEPAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: POTTER,
APPLICANT: MANNS,
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 926 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: PRIOR APPLICATION DATA:
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                                                                                                                               124
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CITY: PALO ALTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CA
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                                                                                        AKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQ
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mmer: US 08/387,156
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Indels Length

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RESULT 11 US-09-124-491-6

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APPLICANT: POTTER, ANDREW A.
TITLE OF INVENTION: PASTEURELLA
COMPOSITIONS AND USES THEREOF
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Best Local
                                      Matches
                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 504,850
FILING DATE: 05-APR-1990
APPLICATION NUMBER: 335,018
FILING DATE: 07-APR-1989
Q ID NO:3:
                                                                                                                                                                                     NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
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                                                                                                                                                                   APPLICATION NUMBER: US/0
FILING DATE: 09-FEB-1993
                  15
                                               Local Similarity
                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                           FGTANSVSSNALQPITQPTQGI 922
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                                                                                                                                                                                                                                                                                                                                                                    FSDSNLKDLTFEKVKHNLVI-TNSKKEKVTTQNWFREADFAKEVPNYKATK-DEKIEEII
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                 LNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT 72
LSFPKTGAKKIILYIPQNYQYDTEQGNGLQDLVKAAEELGIEVQREERNNIATAQTSLGT
                                       Conservative
                                     50.1%; Sco
50.0%; Pro
ative 174;
                                                                                                                                                                             US/08/15
                                                                                                                                                                                                                                                                                        917
                                      Score 2326.5; DB 6
Pred. No. 2.6e-174;
'4; Mismatches 262;
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                                                           6,
                                        Indels
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                                                                      Patent No. 5708155
                                                              GENERAL INFORMATION:
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    SEQUENCES:
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APPLICANT: POTTER, A APPLICANT: REDMOND, APPLICANT: HUGHES, H TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                  Application US/08455970A
                                                                      POTTER, ANDREW A.
                                                    REDMOND,
 D, MARK J.
, HUW P.A.
: ENHANCED
: CHIMERAS
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                      IMMUNOGENICITY USING
                      LEUKOTOXIN
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LENGTH: 936 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-CCT-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                              183 IKGLGTLGDKLKNIGGLDKAGLGLDVISGLLSGATAALVLADKNASTAKKVGAGFELANQ
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/455,970A
FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 285 HAM CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                  73 VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 9001-0016.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: ROBINS, ROBERTA L. REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
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SVLAGMDLDEAL-QNNSNQHALAKAGLELTNSLIENIANSVKTLDEFGEQISQFGSKLQN
                                         KFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGS
                                                                                                 VSGITGVISTILQYSKQAMFEHVANKIHNKIVEWEKNNHGKNYFENGYDARYLANLQDNM
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(415) 327-3231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 174;
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Pred. No. 2.6e
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                         TELEFAX: (415) 327-323
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                              REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 20 STREET: PALO ALTO CITY: PALO ALTO CALIFORNIA "INTTED ST
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CORRESPONDENCE ADDRESS:
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APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING
TITLE OF INVENTION: CHIMERAS
                                                                                                                                                                 FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                  REGISTRATION NUMBER:
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            943 amino acids
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                                                             GKDGSYITSDQIDKILQDKKDGTYITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL
                                                                                                        FADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTDHKIEQLI
                                                                                                                             DRLFGGKGDDILDGGNGDDFIDGGKGNDLLHGGKGDDIFVHRKGDGNDIITDSDGNDKLS
                                                                                                                                          DRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLA
                                                                                                                                                                      IQYRDYELRKYGYGYGSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGD 724
                                          GQNGERITSKQVDDLI--AKGNGKITQDELSKVVDNYELLKHS-KNVTNSLDKLISSVSA
                                                                                    FSDSNLKDLTFEKVKHNLVI-TNSKKEKVTIQNWFREADFAKEVPNYKATK-DEKIEEII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/455,970A
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
CLASSIFICATION: 424
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APPLICATION NUMBER: US 0:
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
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LENGTH: 951 amino acids
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YAERFKKLGYDGDNLLAEYQRGTGTIDASVTAINTALAAIAGGVSAAAAGSVIASPIALL
                                                                VVGNITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSLES
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285 HAMILTON AVENUE,
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                                  GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL 900
                       GQNGERITSKQVDDLI--AKGNGKITQDELSKVVDNYELLKHS-KNVTNSLDKLISSVSA 895
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Search completed: September 11, 2002, 08:59:25 Job time: 208 sec

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Result
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Million cell updates/sec
                                                          Leukotoxin protein
Bovine IL-2/LKT ch
Recombinant leukot
Recombinant leukot
                                                                                                                                         M. bovis Dalton 2d
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Bovine IL-2/Pasteu
Bovine IL-2 - LKT
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Seavocoviii carrier	20100000	2		19.0	0 47
I pulso to via contribut	200	3	200	10.	0
Gonadotropin relea	AAY58133	21	695	19.4	. 901
Leukotoxin/gonadot	AAY58361	21	695	19.4	901
LKT-GnRH chimeric	AAW79573	19	695	19.4	901
LKT-GnRH chimeric	AAW79570	19	544	•	904.5
Pasteurella haemol	AAE04637	22	450	5	1159.5
Enterohaemorrhagic	AAR86998	17	758	७.	1380.5
Pasteurella haemol	AAE04636	22	809	۳	1464.5
LhaA (low homology	AAR76991	16	1023	7.	1731
A. pleuropneumonia	AAY51406	21	1022	8	1767.5
ApxIA protein. Ac	AAW22152	18	1022	œ	1767.5
₽.	AAR54781	15	1244	1	1928
A. pleuropneumonia	AAY51412	21	1049	7	1928
~	AAW22159	18	1049	1.	1928
A. pleuropneumonia	AAY51410	21	956	8	2240.5
ApxIIC protein. A	AAW22156	18	956	8	2240.5
APPA haemolysin an	AAR12561	12	956	8	2240.5
P. suis leukotoxin	AAW07637	17	934	9	2301.5
Rotavirus VP4-leuk	AAR34548	14	951	9.	2312.5
=	AAR15159	12	953	9.	2313
P. haemolytica tru	AAW03945	17	926	9.	2317.5
Leukotoxin 352 enc	AAR10889	12	924	9.	2317.5
GnRH-leukotoxin ge	AAR34547	14	936	9	2318.5
Somatostatin-leuko	AAR34546	14	943		2323.5
urella hae	AAE04638	22	953	0	2325
PtxA protein of Pa	AAR60072	15	953	0	2325
105kD PTX protein	AAR07167	11	953	0	2325
Bovine gamma-IFN/P	AAB21074	21	1069	50.1	2326.5
Chimeric protein #	AAW13867	18	1069	0.	2326.5
Bovine IFNgamma/LK	AAR52748	15	1069	0	2326.5
LKT-GnRH chimeric	AAW79569	19	977	0	2326.5
LKT-GnRH protein f	AAW03942	17	977	0	2326.5
W	95	19	926	50.1	2326.5
Recombinant leukot	AAR50291	15	926	50.1	2326.5

ALIGNMENTS

RESULT AAB62110 Moraxella; antigen; immune response; infection; RTX toxin; vaccine; antibacterial; A subunit. M. bovis Dalton 2d RTX toxin A subunit. AAB62110 standard; Protein; WO200116172-A1. Moraxella bovis. AAB62110; (CSIR) COMMONWEALTH SCI & IND RES (UYME) UNIV MELBOURNE. 31-AUG-1999; 31-AUG-2000; 2000WO-AU01048 08-MAR-2001. 29-MAY-2001 (first entry) \vdash 99AU-0002571. 927 A ORG

Farn

J,

Strugnell R,

WPI; 2001-235092/24. N-PSDB; AAF57290.

Novel Moraxella bovis antigen useful in compositions for raising immune response in an animal, has protease, lipase or hemolysin activity

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{\tt rtetiqyrdyelrkvgygyqstdnlksveevigsqfndvfkgskfndifhsgegddlldg}
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pred. No. 2.4e-294;
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Db Qy

8 173

 Query Match Best Local Matches 46

Similarity

50.2%;

Score 2334; DB 18; Pred. No. 1.1e-143; 5; Mismatches 263;

Length

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26;

Gaps

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Conservative

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                                                                      AAW13866 and AAW13867 represent immunogenic chimeric proteins of the invention. This sequence represents a chimeric protein containing the bovine interleukin-2 (IL-2) sequence and a leukotoxin sequence. The chimeric proteins of the invention comprise a cytokine, selected from II-2 and gamma interferon (gamma IFN), linked to at least one RTX toxin upitope (preferably the sequence shown in AAW13865). The RTX toxin used to provide the epitope sequence is preferably a leukotoxin, especially the full-length Pasteurella haemolytica leukotoxin. Alternatively, the leukotoxin is a truncated leukotoxin lacking leukotoxic activity, especially KT352. The chimeric proteins can be used for the production if vaccines against respiratory diseases such as pneumonia, particularly fibrinous pneumonia caused by P.haemolytica, including shipping fever in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-DEC-1993;
22-AUG-1990;
16-OCT-1991;
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(UYSA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campos
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Bovine IL-2; interleukin-2; leukotoxin;
             Bovine IL-2/Pasteurella haemolytica leukotoxin fusion protein
                              19-DEC-2000
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LKT;
respiratory disease;
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Best Local
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22-JUL-1996;
22-AUG-1990;
16-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                immunogenic chimeric protein that comprises gamma-interferon (gamma-IFN) or an active fragment thereof, linked to an epitope of a Pasteurella haemolytica leukotoxin (LKT). Pasteurella species, especially Pasteurella haemolytica, are responsible for respiratory diseases in a range of agricultural animals, most particularly cattle, but also sheep, pigs, horses and fowl. Shipping fever is the most economically important respiratory disease associated with Pasteurella species, affecting 15-30% of exposed cattle and resulting in a 2-5% mortality rate in the exposed population. The vaccine composition of the invention is is useful for preventing or ameliorating respiratory diseases such as pneumonia, particularly shipping fever pneumonia, in livestock. The present sequence represents a fusion protein comprising bovine interleukin-2 (IL-2) and Pasteurella haemolytica leukotoxin, which may also be appeared to the composition of the composition of the composition of the present sequence represents a fusion protein comprising bovine interleukin-2 (IL-2) and Pasteurella haemolytica leukotoxin, which may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein comprising gamma-interferon and leukotoxin Pasteurella haemolytica
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                                                                                                                                                                                                                                                                                                                                                                                       also be used as an anti-Pasteurella vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campos
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                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1;
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TLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAK
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                                                      LGSTISQAKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAA
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465; Conserv
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Pasteurella
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GEIGY CANADA
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96US-0681479.
90US-0571301.
91US-0777715.
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175; Mismatches
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1.1e-143;
hes 263;
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Matches 464
                                                                                         One or more biologically pure antigenic determinants of the leukotoxin protein comprising of at least six amino acids is a component of a new vaccine for animals. The vaccine elicits an enhanced immune response after challenge with Pasteurella haemolytica. The vaccines other component is a bacterial free culture supernatant derived from a culture of Pasteurella
                                                                                                                                                   Claim 1; Figure 1; 40pp; English.
                                                                                                                                                                  Vaccine for preventing Pasteurella haemolytica infections contains leukotoxin protein antigenic determinants and P. haemolytica culture supernatant
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monoclonal; polyclonal; antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovine; interleukin-2; IL2; P. haemolytica; leukotoxin; ltka; chromosome walking;, fusion protein; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a fusion between bovine interleukin-2 (IL2) and Pasteurella haemolytica leukotoxin (LTR). The leukotoxin gene, ltkA, was isolated from a gene library of P. haemolytica by chromosome walking. Immunogenic fusion proteins such as this can be used in vaccine compositions. It can also be used to raise mono-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leukotoxin -
antibodies
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16-OCT-1991;
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                                                                                 HANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAV
  AYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDG
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464; Conservative
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SASKATCHEWAN.
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91US-0777715.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n proteins of gamma-interferon and immunogenic in vaccines and to raise monoclonal and polyclonal
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04-JUN-1992;
29-MAR-1993;
29-MAR-1993;
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Rioux C
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N-PSDB; AAQ51086.
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                                                                                                                                                                                                                                       Pasteurella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGKRTETIQYBDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDL 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETK
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                                           Theisen
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heisen M;
                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                           SASKATCHEWAN
                                                                                              92US-0865050.

92US-0893424.

92US-0893426.

92US-0038287.

93US-0038288.

93US-0038719.
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Rioux (
                                                                                                                 The hmb gene encoding the haemin-binding protein was expressed in E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene lkth coded for by plasmid phA352. The hmb gene fragment was taken from pRAP504 and starts at the codon for the 33 rd amino acid residue of ORF1. The haemin binding protein can be used in vaccines for preventing or treating H. sommus infections, which cause thromboembolic
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See also AAR42370-86.
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Query Match Best Local Similarity

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50.1%; Score 2326.5; 50.0%; Pred. No. 2.86 tive 174; Mismatches

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Rioux C
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See also AAR42370-86
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92US-0893424.
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RESULT 10
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pr comprise sub-unit antigens from Phaemolytica finbrial protein, pr plasmin receptor, 50 k outer membrane protein and leukotoxin.

XX Disclosure; Fig 5; 92pp; English.

XX EKT352 is 98% homologous with authentic leukotoxin and migrates CC to the same position on gels.

CC The LKT352 gene was prepd. as follows: lktA, an MaeI fragment CC contg, the gene was ligated into the SmaI site of pUCl3 to form CC pAA179. From this, two constructs were made in the ptac-based CC vector, pGH432:lacl digested with SmaI. One, pAA342, consisted of CC the 5' AhaIII fragment. Clone pAA342 expressed a truncated CC the entire MaeI fragment. Clone pAA342 expressed full CC length leukotoxin at very low levels. The 3' end of the lktA gene CC pAA345 was therefore ligated to Styl/BamHI digested pAA342 to CC yield pAA352 contg. the LKT352 sequence. The protein expressed of the P. haemolytica antigens, e.g. fimbrial protein, plasmin CC receptor or 50K outer membrane protein. The vaccine with corresponding fever pneumonia.

CC See also AAR14481, 83,84 and 85.

XX Sequence 926 AA;
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밁 ŞQ рь Q 밁 Š 밁 δÃ ДЬ Ş В Qy Вþ δõ 밁 ρ 밁 δÃ 망 29 Query Match 50.1%; Score 2326.5; DB 1 Best Local Similarity 50.0%; Pred. No. 2.8e-143; Matches 461; Conservative 174; Mismatches 262; 605 483 492 423 432 372 303 183 124 363 252 193 133 67 73 15 LNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT 7 GDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTET VIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALDE TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ kitdgaasstfdltnvvqrigleldnagnvtktketkllaklgegddnvfvgsgtteldg AKGESNIGNKLONL-NESKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNO svlagmdldeal-qnnsnqhalakagleltnslieniansvktldefgeqisqfgsklqn QVTDGEASSKLDFSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG vvgnitkavssyilaqrvaaglsstgpvaaliastvslaisplafagiadkfnhaksles iqtaigltergivlsapqidkllqk---tkagqalgsaesivqnankaktvlsgiqsilg VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG : || : || : || || : | || : | || DB 12; Length 262; Indels 926 25; Gaps 664 602 551 482 431 66 604 542 491 422 362 371 311 242 251 72 12;

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gonadotropin releasing hormone; rotavirus viral protein 4;
carrier protein; lactation; reproduction.
                           Gene libraries of P. haemolytica Al (strain B122) were constructed in lambda gtl1 and pUCl3. Resulting clones were used to transform E. coli and individual colonies were pooled and screened for reaction with serum from a calf which had survived a P. haemolytica infection and that had been boosted with a conc. culture supernatant of P. haemolytica to increase anti-leukotoxin antibody levels. Positive colonies were screened for their ability to produce leukotoxin by incubating cell lysates with bovine neutrophils and measuring the release of lactate dehydrogenase from the neutrophils. A 4kb fragment was obtd. Progressively larger clones were isolated by other colonies were something the colones were something the colones were solated by the colones w
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14-OCT-1992;
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Qy 망 Qγ 밁 20 В Q_{Y} g Qy В δÃ Qy 맑 QY В В Qy В Qy Вb Qy Вþ Qy B Ωy рь Query Match Best Local Matches 461; in paal14. The clone was subjected to restriction enzyme digestion to yield two clones, one expressing truncated leukotoxin peptide at high levels and the other expressing the full length leukotoxin at low levels. The 3' end of the lkth gene from the full length clone was ligated to the truncated gene clone to yield plasmid pha352. The clone was used to produce chimeric proteins by gene fusion with an antigen coding sequence, e.g. the coding sequence of somatostatin, gonadotrophin releasing hormone or rotavirus viral protein 4, i.e. leukotoxin works as a carrier protein to bring about a larger immune response than the antigen alone. Immunisation with these antigens can regulate growth rate, lactation and reproductive efficiency. See also AAR34546-8. Sequence 133 432 303 243 183 124 483 492 423 363 372 193 543 603 605 552 67 Local Similarity 721 725 662 665 73 15 LNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT svlagmdldeal-qnnsnqhalakagleltnslieniansvktldefgeqisqfgsklqn 182 TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ 192 VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132 ${\tt vvgnitkavs} syila qrva {\tt aglsstgpvaaliastvslaisplafagiadkfnhaksles}$ AKGFSNIGNKLONL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNO iqtaigltergivls apqidkllqk---tkagqalgsaesivqnankaktvlsgiqsilgQVTDGEASSKLDFSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG kitdgaasstfdltnvvqrigieldnagnvtktketkiiaklgegddnvfvgsgtteidg gegydrvhysr-gnygaltidatketeggsytvnrfvetgkalhevtsthtalvgnreek GDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTET FADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTDHKIEQLI $\tt drlfggkgddildggngddfidggkgndllhggkgddifvhrkgdgndiltdsdgndkls$ DRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLA ieyr-hsnnqhhagyytkdtlkaveeiigtshndifkgskfndafnggdgvdtidgndgn IQYRDYELRKYGYGYQSTDNLKSVEEYIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGD 926 AA; Conservative 50.1%; 174; Mismatches Score 2326.5; Pred. No. 2.86 es 262; DB 14; Indels Length 926; 25; Gaps 123 242 72 422 431 371 311 251 551 482 491 362 302 661 664 602 604 542 784 720 724

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Matches 461;
                                                                                                                                Haemophilus somnus enriched with iron regulated proteins is new. The vaccine pref. further comprises an immunogenic leukotoxin polypeptide, esp. an immunogenic Pasteurella haemolytica leukotoxin homologous to LKT352. Example 1.2 describes the prodn. of P. haemolytica recombinant leukotoxin from pAA352.

Two expression constructs were made. One, pAA342, contained the 5'-Ahall fragment of the 1tkA gene, while the other, pAA345, contained the entire 1ktA gene. pAA342 expressed a truncated leukotoxin peptide at high levels, while pAA345 expressed full length leukotoxin at very low levels. Therefore, the 3' end of the 1ktA gene was ligated into pAA342, yielding plasmid pAA352. Or new leukotoxin is 98% homologous to authentic
                                                                                                                                                                                                                                                                                                                                               Haemophilus somnus outer membrane protein extract enriched with iron-regulated proteins, opt. contg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR50291 standard;
                                                                                                 NB: the protein sequence in Fig 5 however this protein is described
                                                                                                                                                                                                                                                                                     A vaccine comprising an outer membrane protein (OMP) extract of
                                                                                                                                                                                                                                                                                                                                                                                                                            Harland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pasteurella haemolytica Al
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            Similarity
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           50.1%;
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  174;
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            Score 2326.5; DB 15; Pred. No. 2.8e-143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQ
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svlagmdldeal-gnnsnqhalakagleltnslieniansvktldefgeqisqfgsklqn
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                                                                                                                                    FGTANSVSSNALQPITQPTQGI
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                                                                                                           ftssndsrnvlvaptsmldqsl
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                                                                                                                                                                            GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL
                                                                                                                                                                                                                                                                                                            kitdgaasstfdltnvvqrigieldnagnvtktketkiiaklgegddnvfvgsgtteidg
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                                                                                                                                                                                                              fsdsnlkdltfekvkhnlvi-tnskkekvtiqnwfreadfakevpnykatk-dekieeii
                                                                                                                                                                                                                                                                                                                                     IQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGD
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 (first entry)
                                                 Protein;
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Leukotoxin

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric protein of leukotoxin and gonadotropin releasing hormone useful for, e.g. preparation of vaccines for reduction of incidenc of mammary tumours in mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a recombinantly produced or chemically synthesised leukotoxin 352 (LKT 352)polypeptide, derived from the lktA gene that is present in the plasmid pAA352. This gene produces a truncated protein that has an estimated molecular weight of about 99 kDa and lacks the cytotoxic portion of the molecule. Thus this gene has a higher expression level than that of the full-length molecule. This can be used in the construction of a chimeric protein that comprises a leukotoxin polypeptide, several multimers, and a GNRH sequence. The chimeric protein can be used as a vaccine to help reduce the incidence of mammary tumours in a mammalian individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gonadotropin releasing horn
multimer; vaccine; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7;
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DB; AAV61530.
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                                     AKGESNIGNKLQNL-NESKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNO
                                                                                                                                                                                {\tt svlagmdldeal-qnnsnqhalakagleltnslieniansvktldefgeq is qfgsklqn}
                                                                                                                                                                                                    VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG
                                                                                                                                                                                                                                                                                                                        FAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAVGAPIALL
                                                                                                                                                                                                                                                                                                                                                                                                    461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
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11..924
/note= "Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                   50.1%; Score 2326.5; DB 19; Length 50.0%; Pred. No. 2.8e-143;
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our; Leukotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Recombinant leukotoxin peptide"
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352; LKT
                                                                                                                                                                                                                                                                                                                                                                                                       262;
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                                                                                    Domain
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                                                                                                                                                                                                                 LKT-GnRH protein
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                                                                          /label= GnRH_repeat_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gonadotropin-releasing hormone multimer fusion proteins - we leukotoxin polypeptide for increased immunogenicity, useful antifertility vaccine prodn.
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DB; AAT37176.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-AUG-1997;
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DB; AAV61531.
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The present sequence represents the LKT-GnRH chimeric protein from pCB113. This plasmid contains the LKT-352 polypeptide (AAM79568) fused to four copies of the GnRH peptide. This chimera lacks cytotoxic activity which enables there to be an increase in antigen presentation and thus an optimal immune response. The removal of this region also enables the truncated LKT to be expressed at much higher levels and allows the amount of antigen administered to be reduced. This chimeric protein comprises a leukotoxin polypeptide, several multimers, and a GnR sequence. The chimeric protein can be used as a vaccine to help reduce the incidence of mammary tumours in a mammalian individual.

a GnRH

Chimeric protein of leukotoxin and gonadotropin releasing useful for, e.g. preparation of vaccines for reduction of of mammary tumours in mammals

hormone incidence

Figure 5.1-8;

118pp;

English.

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                                                   GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL 900
                                                                               FADANISDIMIBRTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTDHKIEQLI 840
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                                                                                                                    DRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVLIFRKGDGNDTLYDGTGNDKLA
ftssndsrnvlvaptsmldqsl 917
                                                                    fsdsnlkdltfekvkhnlvi-tnskkekvtiqnwfreadfakevpnykatk-dekieeii
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Search completed: September 11, 2002, 08:58:47 Job time: 191 sec

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RTA_BOVIN
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8 pasteurella
7 pasteurella
1 actinobacil
7 actinobacil
8 bacillus su
7 mycoplasma
2 campylobact
5 bacillus th
0 oryctolagus
2 cricetulus
8 homo sapien
7 drosophila
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4 fervidobact
8 aquifex aeo
0 acidaminoco
0 halobacteri
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homo sapien
pasteurella
methanococc
bacillus sp
salmonella
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and this requires n email	e Swis n Bioi n-prof	ITY: B	DOMAIN: THE THREE INVOLVED IN PORE PTM: PALMITOYLATE	ULAR L THE G , WHIC	N: BAC	S.K., and ex	884-9 TYPE A 36888;	(1989)	TYPE A 10283; S.K., ce of	OM N.A	A1."; un. 55	Strath	OM N.A TYPE A 06837:	75985;	haemolyt roteobact	(Rel.	(Rel.			61.4 61.4 61.4 59.6				•
s statemens a licens to licens	s Institu	MUDIFIED (BI SIMILARITI). SIMILARITY: BELONGS TO THE H	HREE TRAI	OCATION: LY-RICH H IS REQI	TERIAL HI	Engler M pression :2343-23	53 FROM 1 1 / PHL1(PubMed=:	•	PubMed=2707 Chidambaram the Pasteure		7-196	γ (A (A (A (A (A (A (A (A (A (<u> </u>		lytica. acteria;	39, Last erotype A	15, Crea	STANDARD;		1939 1939 1939 1	938		102	
tatement is not remo license agreement (license@isb-sib.ch)	Ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is	THE RTX	RANSMEMBRANE DOMAINS ARE DOMATION BY THE CYTOTOXIN BY LKTC. THE TOXIN ONLY	-!- SUBCELULAR LOCATION: Secreted!- DOMAIN: THE GLY-RICH REGION IS PR -CALCIUM, WHICH IS REQUIRED FOR TA	EMOLYSINS DESE CELL R	.J., Weins of the Pa	N.A. 01; 2185213;		PHLIUI; Med=2707120; ambaram M., En Pasteurella ha	. ;	96(1987).	Shewen P.E.;	3040588:		gamma subdi	annotat 1.	ted)	PRT;	ALIG	MYH6_HUMAN MYH6_MESAU EXE3_HELHO				
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oy and i	restrict	FAMILY.	E BELIEVED TO BE N (BY SIMILARITY) BECOMES ACTIVE W	۵	ATTACK MS NOT				ock G.M.; kin gene			Pasteurella			ellaceae;					P13533 P13539 P13539 P20394	Q02566 P02563	P13540 P79293 P02564		
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Best Local S
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Hemolysis;
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DOMAIN
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REPEAT
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InterPro; IPR003355; RTX_N.
InterPro; IPR003995; RtxA.
                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=SEROTYPE T3;
MEDLINE=94041617; PubMed=8225575;
                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
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                                                                                               Pasteurella haemolytica.
Bacteria; Proteobacteria;
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                                                             SUBCELLULAR LOCATION: Secreted.
DOMAIN: THE GLY-RICH REGION IS PROBABI
CALCIUM, WHICH IS REQUIRED FOR TARGET
       ACTIVITY.

DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY) PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WINDDIFIED (BY SIMILARITY).

SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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;; PS00330; HEMOLYSIN_CALCIUM;
is; Toxin; Cytolysis; Cytotox
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FEHVAN -> LSTLQI (IN REF. 2)
D -> Y (IN REF. 2).
C -- 114118C05F CRC64;
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                                                               CELL-BINDING
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SQUETE TETT TETT
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LKAB_PASHA
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Best Local
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TRANSMEM 229 249 POTENTIAL.
TRANSMEM 297 318 POTENTIAL.
TRANSMEM 381 401 POTENTIAL.
TRANSMEM 381 401 POTENTIAL.
TRANSMEM 381 401 POTENTIAL.
TREPEAT 734 784 6 X REPEATS, GI
REPEAT 743 748 2.
REPEAT 752 757 3.
REPEAT 751 756 4.
REPEAT 770 775 5.
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01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
Leukotoxin from serotype All.
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SEQUENCE
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN_CALCIUM;
Hemolysis; Toxin; Cytolysis; Cytotox.
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Pfam; PF02382; RTX; 1.
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ACTIVITY.

-!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY)
-!- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE V
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01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003355;
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                                                                                                                  "Molecular analysis of the leukotoxin determinants haemolytica serotypes 1 to 16."; Infect. Immun. 61:5001-5007(1993).
-:- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS TH
                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-SERCTYPE All;
MEDLINE-940401617; PubMed-8225575;
Burrows L.L., Olah-Winfield E., L
                                                                                                                                                                                                                                                           Pasteurella haemolytica.
Bacteria; Proteobacteria;
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SUBCELLULAR LOCATION: Secreted.
DOMAIN: THE GLY-RICH REGION IS
CALCIUM, WHICH IS REQUIRED FOR
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Pred. No. 9.1;
1; Mismatches
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                                                                                                         ARE EXOTOXINS THAT ATTACK
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                     SIMILARITY)
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LKAA_PASHA
ID LKAA_PASHA
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DT 01-OCT
DT 30-MCY
DE Leukot
GN LKTA.
OS PASteu
OC Bacter
OC Mannhe
OX NCBI_T
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RP SEQUEN
RX MEDLIN
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Best Local :
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01-OCT-1996
30-MAY-2000
                                                                                                                            MEDLINE-96425875; PubMed-8828217;
Lainson F.A., Murray J., Davies R.C., Donachie W.;
"Characterization of epitopes involved in the neutralization of Pasteurella haemolytica serotype Al leukotoxin.";
Microbiology 142:2499-2507(1996).
-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
SEQUENCE
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InterPro; IPR003355; RTX_N.
InterPro; IPR003995; RtxA.
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                                                                                                                                                                                                                                                                                      STRAIN-SEROTYPE T10;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00313; CABNDNGRPT PRINTS; PR01488; RTXTOXINA.
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                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=75985
                                                                                                                                                                                                                                                                                                                                                                               Mannheimia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leukotoxin
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                           SUBCELULAR LOCATION: Secreted. DOMAIN: THE GLY-RICH REGION IS CALCIUM, WHICH IS REQUIRED FOR ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
      DOMAIN:
                                                                                                                 DEFINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MODIFIED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 (Rel. 34, Created)
6 (Rel. 34, Last sequence up
0 (Rel. 39, Last annotation
from serotype T10.
      THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO
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102206 MW;
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75.0%;
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Pred. No. 9.1;
1; Mismatches
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6 X REPEAT
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                                             PROBABLY INVOLVED IN BINDING TARGET CELL-BINDING OR CYTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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                                             OR CYTOLYTIC
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                                                                                                                                                                                                                                                                  Q00951;
01-APR-1993;
01-APR-1993;
30-MAY-2000;
                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Hemolysin (Cytolysin II) (CLY-IIA) (HLY-IIA)
APPA OR CLYIIA OR HLYIIA OR CYTC.
                                                Actinobacillus suis.";
Infect. Immun. 60:2166-2173(1992).
-!- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.SUI
SECRETED CYTOTOXIN, POSSIBLY THE EXTRACELLULAR
                                                                                                                                             SEQUENCE FROM N.A. STRAIN=3714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
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REPEAT
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Pfam; PF02382; RTX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                           -1- SUBCELLULAR LOCATION: Secreted.
                                                                                                                      Burrows L.L., Lo R.Y
                                                                                                                                                                                                                                                                                                                        HLYA_ACTSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z26247; CAA81206.1; -
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                                                                                                        "Molecular characterization of an
                                                                                                                                 MEDLINE=92267623; PubMed=1587585;
                                                                                                                                                                                    Actinobacillus.
NCBI_TaxID=716;
                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                             Actinobacillus suis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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nes 9; Conserv
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  CALCIUM,
ACTIVITY.
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European Bioinformatics Institute. There a
by non-profit institutions as long as i
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                                                                                                                                                                                                                                                                                                                                                                                          FLLNLNKELQAE 464
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IPR003355;
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75.08;
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                REQUIRED
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Pred. No. 9.1;
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                PROBABLY INVOLVED TARGET CELL-BINDIN
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                CELL-BINDING
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                                                     HEMOLYSIN.
                            IN BINDING
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Best Local Similarity
Taches 9; Conser
                  SEQUENCE FROM N.A.
STRAIN-SEROTYPE 5;
MEDLINE-9012633; PubMed=2693022;
Chang Y.-F., Young R., Struck D.K.;
"Cloning and characterization of a he
(Haemophilus) pleuropneumoniae.";
DNA 8:635-647(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
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REPEAT
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN_0
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                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
30-MAY-20000 (Rel. 39, Last annotation updat
RTX-II toxin determinant A (APX-IIA) (Hemol
(Cytolysin IIA) (CLY-IIA).
APXIIA OR CLYIIA OR HLYIIA OR APPA OR CYTC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00353; hemolysinCabind;
Pfam; PF02382; RTX; 1.
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InterPro; IPR003355; RTX_N.
InterPro; IPR003995; RtxA.
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                                                                                                                                                                                                        Bacteria; Proteobacteria; Actinobacillus.
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                                                                                                                                                                                   NCBI_TaxID=715;
                                                                                                                                                                                                                                            Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         455 FLINLNKELQAE 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY) PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLSELNKELEAE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238
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                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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POTENTIAL.
9 X REPEATS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.54.32.
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                             (Haemophilus subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3415FF1D7ADD4365 CRC64;
                                                               a hemolysin gene from Actinobacillus
                                                                                                                                                                                                                                                                                                                                                                                                              956
                                                                                                                                                                                                                                                                                                       (Hemolysin
                                                                                                                                                                                                                                                                                                                                update)
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Pasteurellaceae;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ISOLATE CVI 13261 / SEROTYPE MEDLINE=92040145; PubMed=1937809;
                                                                                                                                                                                          REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00353; hemolysinCabind; pfam; PF02382; RTX; 1. PRINTS; PR00313; CABNDNGRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: Secreted.
-i- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING O ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cytolysins of Actinobacillus pleuropneumoniae serotype 9.";
Infect. Immun. 59:4497-4504(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gielkens A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smits M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                               REPEAT
REPEAT
REPEAT
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; B33389; B33389.
PIR; S18853; S18853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M30602; AAA87232.1; -. EMBL; X611111; CAA43423.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003355;
InterPro; IPR003995;
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001343;
                                                     BACSU
                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                  PRINTS;
                    P23448;
01-NOV-1991
                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                          Hemolysis;
16-OCT-2001
           01-NOV-1991
                                          FLIG_BACSU
                                                                                               455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY). PTM: PALMITOYLATED BY APXIIC. THE TOXIN ONLY BECOMES ACTIVE WHEN
                                                                                                                   1 FLSELNKELEAE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MODIFIED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCT. IMMUN. 59:4497-4504(1991).
FUNCTION: ONE OF THE VIRULENCE FACTORS OF WHICH SHOWS A WEAK HEMOLYTIC ACTIVITY AND FOR ALVEOLAR MACROPHAGES AND NEUTROPHILS.
                                                                                               FLINLNKELQAE 466
                                                                                                                                       Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                 PR01488; RTXTOXINA.
                                                                                                                                                                                                                                                                                                                                                     PS00330;
                                                                                                                                                                                                                                                                                                                                            Toxin;
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(Rel.
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                                                                                                                                        Conservative
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                                                                                                                                                                                            AA;
                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                     HEMOLYSIN_CALCIUM;
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102531 MW;
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                                                                                                                                                  75.48;
75.08;
 Last sequence update)
Last annotation updat
                      Created)
                                                                                                                                        Score 43; DB Pred. No. 9.1; Mismatches
                                                                                                                                                                                                                                                                                                                                   Palmitate.
                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                            CALCIUM; 1.
Cytotoxin;
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                                                                                                                                                                                                                                                                                        POTENTIAL.
8 X REPEATS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9;
                                           338
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                                                                                                                                                    DB 1;
9.1;
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There are no rest
ng as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kamp E.M.,
                                                                                                                                           2;
                                                                                                                                                             Length 956;
                                                                                                                                                                                                                                                                                                                                              Calcium;
                                                                                                                                                                                              CRC64;
                                                                                                                                           Indels
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OR CYTOLYTIC
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Bacillus subtilis. Bacteria; Firmicutes;

Flagellar motor switch

protein flig

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RESULT
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R HSSP; O9WY63; 19C7.

R HSSP; O9WY63; 19C7.

R HSSP; O9WY63; 19C7.

R SubtList; BG10241; filg.

DR InterPro; IPR000090; F1g_Motor_F11g.

DR Pfam; PF01706; F11G-C; 1.

DR PFAWYS; PR00954; FLGMOTORFLIG.

PRAVYS; PR00954; FLGMOTORFLIG.

PRAVYS; PR00954; FLGMOTORFLIG.

PRAVYS; PR0954; FLGMOTORFLIG.

PRAVYS; PR0954; FLGMOTORFLIG.

PRAVYS; PR0954; FLGMOTORFLIG.

PRAVE TO MEMBRANA SA191 MW; 8C44193BA0ADE58E CRC64;

PR 1; Length 338;

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                    NFM_PIG STANDARD; PRT; 454 AA.
P08552;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament protein)
(Neurofilament medium polypeptide) (NF-M) (Fragment).
                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between
the Euro
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J. Bacteriol. 173:3573-3579(1991).

T. Bacteriol: ONE OF THE PROTEINS THAT PROPOSED TO BE LOCATED AT THE BASE INTERACTS WITH CHEMOTAXIS PROTEINS CONTACTING COMPONENTS OF THE MOTOR FLAGELLAR ROTATION.
TISSUE-Spinal cord;
MEDLINE-85076594; PubMed-6439558;
Geisler N., Fischer S., Vandekerc
"Hybrid character of a large neur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. entities requires a license agreement (See ) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Albertini A.M., Caramori T., Crabb W.D., Scoffone F., Galizzi A.; "The flam locus of Bacillus subtilis is part of a large operon coding for flagellar structures, motility functions, and an ATPase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91258343; PubMed=1828465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus/Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Membrane-associated SIMILARITY: BELONGS TO THE FLIG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSELNPEVQAE
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Z99112; CAB13495.1;
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8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160
                                                                                                                                                                                                                                                                                Chordata; Craniata; Vert Cetartiodactyla; Suina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus/Clostridium group;
us group; Bacillus.
                                         Vandekerckhove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB
Pred. No. 15;
2; Mismatches
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    neurofilament
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                                                                                                                                                                                                                                                                                                                 Vertebrata;
Plessmann U.,
protein (NF-M
                                                                                                                                                                                                                                                                                Suidae;
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    (NF-M)
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RESULT 9

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Best Local s
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16-OCT-2001 (Rel. 40, L
16-OCT-2001 (Rel. 40, L
Neurofilament triplet M
(Neurofilament medium F
NEF3 OR NEFM OR NFM.
"The bovine neurofilament M subunit has a novel set of KSP repeats normally restricted to NF-H.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L,
AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER
-!- PTM: THERE ARE A NUMBER OF REPEARYS OF THE TRIPEPTIDE K-S-P, NET
PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001
16-OCT-2001
16-OCT-2001
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SEQUENCE
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EMBO J. 3:2701-2706(1984).
-i- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, N
AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
                                                                                                                                                                                                           Hill W.D., Zha Gearhart D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
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-!- SIMILARITY: BELONGS TO THE INTERNEDIATE FILAMENT FAMILY.
PIR: A05075; OPPOM.
                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                            Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFM_BOVIN
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                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
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Last annotation update)
M protein (160 kDa neurofilament protein)
polypeptide) (NF-M) (Fragment).
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O-LINKED
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LINKER 2.
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                                                                                                                                                                                                                                       T.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFM_RAT STANDARD; PRT; 845 AA.
P12839; Q63370;
01-CCT-1989 (Rel. 12, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament
(Neurofilament medium polypeptide) (NF-M).
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                    SEQUENCE FROM N.A.
STRAIN-WISTAR;
MEDLINE-92332596; PubMed-1321159;
Kelly B.M., Gillespie C.S., Sherm
                                                                                                                                                                          MEDLINE-87282618; PubMed-2441012;
Napolitano E.W., Chin S.S.M., Colman D.R.,
"Complete amino acid sequence and in vitro
the middle molecular weight neurofilament
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                      NEF3 OR NEFM OR NFM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE OF AXONAL CALIBER (BY SIMILARITY).

PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION (BY
                                                                                                                                                     Neurosci.
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een the Swiss Institute of Bioinformatics and the EN
European Bioinformatics Institute. There are no resti
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LINKER 12.
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8 X 13 AA TANDEM REPEATS.

8 B8477D855560AC3F6 CRC64;
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J. Cell Biol. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYDRATE-LINKAGE SITES
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                                                                                                                                                                                                                                                                                                                                                                  EMBL; M18628; AAA41696.1;
EMBL; Z12152; CAA78136.1;
GlycoSuiteDB; P12839; ---
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O-linked N-acetylglucosamine moieties on ne
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SIOL. Chem. 268:16679-16687(1993).

FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE OF REURONAL CALIBER. AND H WHICH ARE INVOLVED IN THE MAINTENANCE K-S-P, NFM IS PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPETTIDE K-S-P, NFM IS PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS FORMATION OF THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE MAINTENANCE THOUGHT THAT PROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF AXONAL CALIBER.

DTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTOF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ntification of six phosphorylation region of the rat neurofilament pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-profit
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                                                                                                                                                                                                                                                                                                                                                         IPR001664; IF.
                                                                                                                                                                                                                                                                                                                                                                                                                 email to license@isb-sib.ch).
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O-LINKED (GLCNAC).
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Best Local
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P08553; Q61961;
01-AUG-1988 (Rel. 08, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2101 (Rel. 40, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Levy E., Liem R.K.H., D'Eustachio P., Cowan N.J "Structure and evolutionary origin of the gene the middle-molecular-mass neurofilemone."
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                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-slb.or send an email to license@isb-sib.ch).
                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                            EMBL; X05640; CAA29127.1; -. EMBL; M20481; AAA39815.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      between
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MEDLINE-87158637; PubMed-3103856;
Julien J.-P., Meyer D., Flavell D., Hu
"Cloning and developmental expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-87246694; PubMed-3036526;
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                                                                                                                                             PROSITE;
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                                                                                                                 intermediate filament;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION. SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               middle-molecular-mass neurofilament . J. Biochem. 166:71-77(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute.
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FUNCTION: NEUROFILAMENTS
AND H WHICH ARE INVOLVED
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PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE
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                                                                                                                                                                                    S00030; S00030.
MGI:97314; Nfm.
rPro; IPR001664; IF.
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IN THE MAINTENANCE OF NEURONAL CALIBER
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                                                                                                                    Neurone;
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There are no restrictions
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01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament medium polypeptide) (NF-M).
                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restitute the European Bioinformatics Institute.
                                                                                                                                                                                                                         +
                                                                                                                                                                                                                                                                                   Zopf D., Hermans-Borgmeyer I., Gundelfinger E.D., Betz H.; "Identification of gene products expressed in the developing visual system: characterization of a middle-molecular-weight
                                                                                                                                                                                                                                                                                                                MEDLINE=88112814; PubMed=3123320;
Zopf D., Hermans-Borgmeyer I., Gu
                                                                                                                                                                                                                                                                                                                                                                               Zopf D., Dineva B., Betz H., Gundelfinger E.D.; "Isolation of the chicken middle-molecular weight (NF-M) gene and characterization of its promoter."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                              Genes
                                                                                                                                                                                                                                                                        neurofilament cDNA.";
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                                                                                                                                                                                                                                                                                                                                                                     Nucleic
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ETUNCTION: NEUROPILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M FUNCTION: NEUROPILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALLEER. PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NEW PHOSPHORYLATED ON A NUMBER OF THE SERIUES IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF NEW RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE.
                                                                                              OF AXONAL CALIBER.

PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FOTHE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H)
OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H)
LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY
COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
SIMILARITY: BELONGS TO THE INTERNEDIATE FILAMENT FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=87275853; PubMed=3608989; Myers M.W., Lazzarini R.A., Lee V.M.-Y., Schlaepfer W.W., "The human mid-size neurofilament subunit: a repeated prot sequence and the relationship of its gene to the intermedificament gene family.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF ONE OF THE 13 RESIDUE MEDLINE=88158120; PubMed=2450354; Lee V.M.-Y., Otvos L. Jr., Carden
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Lazzarini R.A.;
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X05558; CAA29073.1;

LAZ7040; AZ7040.

S08061; S08061.

S15762; S15762.
             TABLI ACAD. Sci. U.S.A. 85:1998-2002(1988).
FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THEE IF PROTEINS: L, METONOMENT UNITED AND HEALT ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER, PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM PHOSPHORYLATED ON A NUMBER OF THE SERINGS IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF THE RESULTS IN THE FORMATION OF THE TRIPEPTION OF THE TRIPETTION OF THE TRIPETTI
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Last annotation update)
M protein (160 kba neurofilament protein)
polypeptide) (NF-M) (Neurofilament 3).
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LINKER 12.
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Catarrhini; Hominidae
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Matches 7
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01-OCT-1996
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
SEQUENCE
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                                       SEQUENCE FROM N.A.
MEDLINE-9329320; PubMed-8478098;
Chang Y.-F., Ma D.-P., Shi J., Chengappa M.M.;
"Molecular characterization of a leukotoxin ge
haemolytica-like organism, encoding a new memb
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Bacteria; Proteobacteria; gan
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P55123;
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PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FORM: PHOSPHORYLATION SEEMS TO PLAYEPTIDES (NF-M AND NF-H) OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H) LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION. SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
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26; IF; 1.
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LINKER 12.
COIL 2A.
LINKER 2.
COIL 2B.
6 X 13 AA TANDEM RE
0-LINKED (GLCNAC)
0-LINKED (GLCNAC)
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LINKER 1.
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ROD.
TAIL.
COIL
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subdivision; Pasteurellaceae;
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            CYTOTOXIC
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MBL outstation -
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01-NOV-1997
16-OCT-2001
SEQUENCE FROM N.A.

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
REPEAT
SEQUENCE
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REPEAT
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                                                                                                                                                                                                       Archaea; Euryarchaeota; Methanococcus.
                                                                                                                                                                                                                                                                         Hypothetical aldolase MJ1418.
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InterPro; IPR003355;
InterPro; IPR003995;
                                                                                                                                                                                                                                                  Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                  Q58813;
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DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY)
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SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY
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DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE
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. 35, Last sequence update)
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. 40 class II protein MJ141
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POTENTIAL.
POTENTIAL.
7 X REPEATS
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Pred. No. 44;
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Science 273:1058-1073(1996).
-i- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
-i- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ARAD/.
SUBFAMILY. STRONG, TO E.COLI YGBL AND H.INFLUENZAE HI1012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scott J.L., Geoghagen N.S.M., Weldman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kalne B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus fannaschii.":
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                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for com
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or send an email to license@isb-sib.ch).
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A; Reference number: A30169; A; Accession: B30169

R;Highlander, S.K.; Chidambaram, M.; Engler, M.J.; Weinstock, G.M.
DNA 8, 15-28, 1989
A;Title: DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster.
A;Reference number: A30169; MUID:89210283

N;Alternate names: lktA protein C;Species: Pasteurella haemolytica C;Species: Pasteurella haemolytica C;Date: 12-Oct-1989 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999 C;Accession: B30169; C32051; S29516

leukotoxin A - Pasteurella haemolytica (serotype 1)

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
35	35	<u>3</u> 5	35	36	36	36	36	36	36	36	36	36	36	36	36
61.4	61.4	61.4	61.4	63.2	63.2	63.2	63.2	63.2	63.2	63.2	63.2	63.2	63.2	63.2	63.2
152	150	143	136	1792	955	913	828	557	462	379	235	203	196	196	159
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T02703	S60838	н71970	F97759	T13939	T21612	T25965	S56250	T47128	S52528	DWDXBF	AF2157	н83806	AI1508	AH1149	F96794
hypothetical prote	M protein precurso	hypothetical prote	hypothetical prote	myosin V - fruit f	hypothetical prote	hypothetical prote	probable membrane	heat shock protein	ULA1 protein - yea	2-hydroxyglutaryl-	transcription regu	hypothetical prote	hypothetical prote	hypothetical prote	probable calmoduli

ALIGNMENTS

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A;Description: lyses leukocytes (S;Superfamily: hemolysin A; hemolysin A homology C;Superfamily: hemolysin A; hemolysis; exotoxin; hemolysis; lipoprotein; tandem rep C;Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem rep F;238-784/Domain: hemolysin A homology <HLYA>
F;716-807/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F;554/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 947-953 <STR>
A;Residues: 947-953 <STR>
R;Lo, R;C.; Strathdee, C.A.; Shewen, P.E.
Infect. Immun. 55, 1987-1996, 1987
A;Title: Nucleotide sequence of the leukotoxin genes
A;Reference number: S29515; MUID:87306837
A;Accession: S29516
В
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                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: lktA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-741,'D','743-953 <LOR>
A;Residues: 1-741,'D','743-953 <LOR>
C;Comment: This organism causes bovine pneumonic pasteurellosis (shipping fever).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-953 <HIS>
A;Residues: 1-953 <HIS>
R;Strathdee, C.A.; Lo, R.Y.C.
J. Bacteriol. 171, 916-928, 1989
J. Title: Cloning, nucleotide sequence, and A;Reference number: A32051; MUID:89123172
A;Accession: C32051
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C;Function:
A;Description: attacks cell membranes and causes cell lysis
C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat;
F;240-786/Domain: hemolysin A homology <HLYA>
F;718-809/Region: 9-residue repeats
F;718-726/Region: repeat
F;727-735/Region: repeat
F;736-744/Region: repeat
F;745-753/Region: repeat
F;727-780/Region: repeat
F;727-780/Region: repeat
F;727-780/Region: repeat
F;727-80/Region: repeat
F;721-89/Region: repeat
F;721-89/Region: repeat
F;721-890/Region: repeat
F;556/Binding site: palmitate (Lys) (covalent) #status predicted
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A;Accession: S34237
A;Cross-references: GB:M24197; GB:M34943; GB:M34944
R;Lainson, A.F.; Aitchison, K.D.; Donachie, W.
submitted to the EMBL Data Library, June 1993
A;Reference number: S34235
A;Accession: S34237
toxin II - Actinobacillus pleuropneumoniae
N;Alternate names: cytolysin II; RTX-toxin II (ApxII)
C;Species: Actinobacillus pleuropneumoniae
C;Date: 09-Mar-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
C;Accession: B33389; S18853; B43599
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A;Title: Secretion and expression of the Pasteurella haemolytic A;Reference number: A35254; MUID:90236888
A;Accession: A35254
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R;Lainson, A.F.; Aitchison, K.; Donachie, W.
Submitted to the EMBL Data Library, September 1993
A;Description: DNA sequence of the leukotoxin A gene
A;Reference number: S37145
A;Accession: S37145
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A; Residues: 723-955 <LA3>
A; Cross-references: EMBL: 2
A; Experimental source: ser
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C;Accession: S37145; A35254; S34237; S34235
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A; Residues: 745-955 <LA2>
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A;Title: Cytolysins of Actinobacillus pleuropneumoniae serotype A;Reference number: A43599; MUID:92040145 A;Accession: B43599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross references: EMBL:X61111; NID:g38939; PIDN:CAA43423.1; PID:g38941 R;Smits, M.A.; Briaire, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Gielken Infect. Immun. 59, 4497-4504, 1991
A;Description: attacks cell membranes and causes cell lysis C;Superfamily: hemolysin A; hemolysin A homology c;Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; F;243-787/Domain; hemolysin A homology <HLYA>
F;719-801/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F;557/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; F;243-787/Domain: hemolysin A homology <HLYAF F;243-787/Domain: hemolysin A homology <HLYAF F;719-801/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X) F;557/Binding site: palmitate (Lys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Smits, M.A.; Briaire, J.; Jansen, R.; Smith, H.E.; submitted to the EMBL Data Library, July 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Cloning and characterization of a A; Reference number: A33389; MUID:90126233 A; Accession: B33389
                                                                                                                                                               A;Note: sequence extracted from NCBI backbone (NCBIN:104212, NCBIP:104211) C;Comment: This organism causes acute fatal septicemia in young pigs. C;Function:
                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-956 <BUR>
A; Experimental source: isolate 3714
                                                                                                                                                                                                                                                                                                            Infect. Immun. 60, 2166-2173, 1992
A;Title: Molecular characterization of
A;Reference number: A43834; MUID:922676
A;Accession: A43834
                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: ashA protein; cytolysin II; RTX-toxin C;Species: Actinobacillus suis C;Date: 31-Dec-1993 #sequence_revision 08-Nov-1996 #text_C;Accession: A43834
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A; Residues: 1-27;948-956 <SM2>
A; Cross-references: GB:X61111; NID:g38939
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A; Residues: 1-956 <SMI>
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DNA 8, 635-647, 1989
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Best Local
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C;Accession: rnvvv;
R;Linial, M.; Scheller, R.H.
J. Neurochem. 54, 762-770, 1990
A;Title: A unique neurofilament from Torpedo electric
A;Title: A unique neurofilament grom Torpedo electric
                                                                                                                                                                                                                                                                      F:98-194/Région: coil Ib
F;217-367/Region: coil II
F;410-597/Region: glutamic acid-rich
F;598-674/Region: 6-residue repeats
F:598-674/Region: 6-residue repeats
F:675-784/Domain: carboxyl-terminal #status predicted
F:616,622,628,634,640,646,652,658,670/Binding site: ph
RESULT 7
B42365
flagellar motor
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Molecule type: mRNA
A:Residues: 1-784 <LIN>
C:Comment: Neurofilaments are a subgroup of intermediate filaments which are expressed
C:Superfamily: cytoskeletal keratin
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C:Species: Torpedo californica (Pacific electric ray)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 27-Oct-1995
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A;Molecule type: mRNA
A;Residues: 1-913 <GER>
A;Cross-references: EMBL:U85970; PIDN:AAB53390.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Sequence and expression pattern of two forms A;Reference number: Z26090 A;Accession: T52485
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switch protein flig - Bacillus subtilis
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75.0%;
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Pred. No.
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Pred. No. 25;
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A;Cross-references: EMBL:x56049; NID:g39904; PIDN:CAA39521.1; PID:g39905
C; Ravevedo, V.; Cardwell, B.; Capuano, V.; Carter, N.M.;
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galizci, A.; C.; Rocha, C.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinc, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maly, M.; Ogawa, K.; Ogwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portett, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scan, A; Authors: Schleich, S.; Schroetet, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scan, A; Stan, A; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurofilament triplet M protein - pig (fragments)
N;Alternate names: 160K neurofilament protein; NF-M(medium) protein; type IV IF
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31:Mar-1988 #sequence_revision 02-Jul-1998 #text_change 10-Jul-1998
C;Accession: A05075; S02570
R;Geisler, N.; Fischer, S.; Vandekerckhove, J.; Plessmann, U.; Weber, K.
EMBO J. 3, 2701-2706, 1984
A;Title: Hybrid character of a large neurofilament protein (NF-M): intermediate
A;Reference number: A05075; MUID:85076594
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: 69624; S14495
C;Accession: A.M.; Caramori, T.; Crabb, W.D.; Scoffone, F.; Galizzi, A.
J. Bacteriol. 173, 3573-3579, 1991
A;Title: The flaA locus of Bacillus subtilis is part of a large operon codi
A; Experimental source: spinal cord C; Superfamily: cytoskeletal keratin C; Keywords: blocked amino end; coil
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C; Keywords: flagellar rotation
                                                                                                                              A; Molecule type: protein
A; Residues: 438-450; 455-459; 460-475; 476-514; 515-532
                                                                                                                                                                                                                  A; Title: Location and sequence characterization of the major phosphorylation sites on A; Reference number: S02570; MUID:87304852
A; Accession: S02570
                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: spinal cord R; Geisler, N.; Vandekerckhove, J.; Weber, FEBS Lett. 221, 403-407, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 1-454 <GEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A05075; A; Accession: A05075
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A;Experimental source: strain 168
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A; Residues: 1-338 <ALB>
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A;Accession: B42365
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Best Local
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72.7%;
coiled coil; intermediate filament; phosphoprotein
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Pred. No. 41;
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neurofilament medium protein - goldfish
C;Species: Carassius auratus (goldfish)
C;Species: C1-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 13-Aug-1999
C;Accession: I50479
R;Glasgow, E; Hall, C.M.; Schechter, N.
J. Neurochem. 63, 52-61, 1994
A;Title: Organization, sequence, and expression of a gene encoding goldfish neuropersion: I50479
A;Accession: I50479; MUID:94267484
A;Accession: I50479
A;Accession: I50479
A;Cossion: I50479
A;Rotatus: preliminary; translated from GB/EMBL/DDBJ
A;Rotatus: preliminary; translated from GB/EMBL/DDBJ
A;Rotatus: 1-798 <GLA>
A;Rosidues: 1-798 <GLA>
A;Cross-references: GB:L09742; NID:9213019; PIDN:AAA72341.1; PID:9213020
C;Genetics:
A;Introns: 343/3; 385/2
C;Superfamily: cytoskeletal keratin
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F;99-412/Domain: alpha helical rod <FCOD>
F;99-412/Domain: alpha helical rod <FCOD>
F;438-454,455-459,460-475,476-514/Domain: tail (fragments) #status predicted <TLP1>
F;515-532/Domain: tail (fragment) #status predicted <TLP2>
F;1/Modified site: blocked amino end (Ser) (probably acetylated) #status experiments
F;456,462,465,479/Binding site: phosphate (Ser) (covalent) #status experimental
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-845 <NAP>
A; Residues: 1-845 <NAP>
A; Coss-references: EMBE:M18628; NID:9205687; PIDN:AAA41696.1; PID:9205688
A; Cross-references: EMBE:M18628; NID:9205687; PIDN:AAA41696.1; PID:9205688
R; Kelly, B.M.; Gillespie, C.S.; Sherman, D.L.; Brophy, P.J.
J. Cell Biol. 118, 397-410, 1992
A; Title: Schwann cells of the myelin-forming phenotype express neurofilament protein
A; Reference number: S25712; MUID:92332596
A; Accession: S25712; MUID:92332596
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-17,19-21,'P',23-204,'L',206-500,'E',501-845 <KEL>
A;Cross-references: EMBL:212152; NID:g56751; PIDN:CAA78136.1; PID:g56752
A;Cross-references: EMBL:A112152; NID:g56751; PIDN:CAA78136.1; PID:g56752
B;Xu, Z.S.; Liu, W.S.; Willard, M.B.
J. Biol. Chem. 267, 4467-4471, 1992
                                                                                                                                                                                                                                                                                                                                                                               A;Title: Complete amino acid sequence and A;Reference number: A45669; MUID:87282618 A;Accession: A45669
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Best Local :
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Best Local :
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7; Conserva
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58.3%;
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58.3%;
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Pred. No.
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A;Reference number: A42393; MUID:92165797
A;Accession: A42393
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 411-500,'E',501-843,'D' <XUI>
A;Note: sequence extracted from NCBI backbone (NCBIP:83873)
C;Superfamily: cytoskeletal keratin
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F;412-849/Domain: tail <TAI>
F;412-849/Domain: tail <TAI>
F;412-849/Domain: tail <TAI>
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C; Superfamily: cytoskeletal keratin
C; Keywords: coiled coil; intermedia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Biochem. 166, 71-77, 1987
A;Title: Structure and evolutionary origin of the gene encoding
A;Reference number: S00030; MUID:87246694
A;Accession: S00030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurofilament triplet M protein - mouse
N;Alternate names: 160K NF protein; NF-M
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
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C; Accession: S00030
                                                                    A;Cross-references: EMBL:X17102; NID:g63688; PIDN:CAA34958.1; R;Zopf, D.; Dineva, B.; Betz, H.; Gundelfinger, E. submitted to the EMBL Data Library, November 1989
                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-858 <200>
                                                                                                                                                                                                          R;Zopf, D.; Dineva, B.; Betz, H.; Gundelfinger, E.D.
Nucleic Acids Res. 18, 521-529, 1990
A;Title: Isolation of the chicken middle-molecular weight neurofilament (NF-M)
A;Reference number: S15762; MUID:90174973
                                                                                                                                                                                                                                                                                     neurofilament triplet M protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
C;Accession: S15762; S08061; A27040
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S15762
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A; Residues: 1-849 <LEV>
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A; Molecule type: DNA
A; Residues: 1-355,368-858
                                  A; Reference number: S08061
A; Accession: S08061
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Best Local :
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Best Local 9
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Biochem. 166,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R.K.H.; d'Eustachio, P.;
166, 71-77, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NID: g53357; PIDN: CAA29127.1;
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Pred. No. 1.1e
3; Mismatches
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1.1e+02;
2;
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                                                                                                                     PID:g63689
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gene

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neurofilament triplet M protein - human
N;Alternate names: NF-M (medlum) protein
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: A27864; A30157
                                                                                                                                                                                                                               RESULT
A64477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 360/3; 402/2
C;Superfamily: cytoskeletal keratin
C;Keywords: coiled coil; phosphoprotein
F;615,628,641,654,680/Binding site: phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:Y00067; NID:g35045; PIDN:CAA68276.1; PID:g35046
R;Lee, V.M.Y.; Otvos Jr., L.; Carden, M.J.; Hollosi, M.; Dietzschold, B.; Lazzarini, R.P.
Proc. Natl. Acad. Sci. U.S.A. 85, 1998-2002, 1988
A;Title: Identification of the major multiphosphorylation site in mammalian neurofilamen
A;Reference number: A30157; MUID:88158120
A;Contents: annotation; phosphorylation sites
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Myers, M.W.; Lazzarini, R.A.; Lee, V.M.Y.; Schlaepfer, W.W.; Nelson, D.L. EMBO J. 6, 1617-1626, 1987
A;Title: The human mid-size neurofilament subunit: a repeated protein sequence A;Reference number: A27864; MUID:87275853
A;Accession: A27864
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Best Local Similarity
Themes 7; Conserve
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C;Superfamily: cytoskel
C;Keywords: coiled coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Identification of gene products expressed in the developing cl
A;Reference number: A27040; MUID:88112814
A;Accession: A27040
A;Molecule type: mRNA
A;Residues: 350-546, 'R',548-858 <203>
A;Cross-references: GB:X05558; NID:g63685; PIDN:CAA29073.1; PID:g63686
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-916 < MYE>
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R;Zopf, D.; Hermans-Borgmeyer, I.; Gundelfinger,
Genes Dev. 1, 699-708, 1987
                                                                                                                                                                                                                                                                                                                 В
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116 YLEQQNKETEAE 127
                                                                                                                                                                                                                                                                                                                   121 YLEQQNKEIEAE 132
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                                                                                                                                                                                                                                                                                                                                                      FLSELNKELEAE 12
                                                                                                                                                                                                                                                                                                                                                                                          h 68.4%;
Similarity 58.3%;
7; Conservative
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58.3%;
                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 2; Lo
Pred. No. 1.2e+02;
3; Mismatches 2;
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Pred. No. 1.1e+02;
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                             Methanococcus
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                                                                                                        Sutton, G.
                         Smith, H.O.; Woese, thanococcus jannaschi
                                                                                     Hurst, M.A.
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Search completed: Job time: 232 sec

September

11,

2002, 09:00:14

В

151

LSEEQKELEAE 161

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Qy
                                                                                                            A;Gene: e12
C;Superfamily: Lactococcus phage bIL170 gene e12 protein
                                                                                                                                 C;Genetics:
A;Gene: e12
                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-211 <CRU>
                                                                                                                                                                                                                                                 A; Description: Sequence and organization of the lactococcal A; Reference number: z14903 \,
                                                                                                                                                                                                                                                                             C;Accession: T03355
R;Crutz-Le Coq, A.M.; Cesselin, B.; Commissaire, J.; submitted to the EMBL Data Library, June 1921
                                                                                                                                                                                                                                                                                                                                 gene e12 protein - Lactococcus phage bIL170
C;Species: Lactococcus phage bIL170
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
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C; Superfamily: L-ribulose-phosphate 4-epimerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-181 <BUL>
                                                                                                                                                                  A;Cross-references: EMBL:AF009630; NID:g3282260; PIDN:AAC27226.1; PID:g3282307
                                                                                                                                                                                                                                    A; Reference number: A; Accession: T03355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:U67582; GB:L77117; NID:g1592064; PIDN:AAB99428.1; PID:g159206
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                                                   Query Match
Best Local
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 2 LSELNKELEAE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                             preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
7; Conserv
                                Similarity
9; Conserv
                                  Conservative
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                                                  66.7%;
81.8%;
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70.0%;
                                Score 38; DB Pred. No. 37; O; Mismatches
                                  0;
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Pred.
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32;
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                                  Indels
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Post-processing: Minimum Match 08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq length: 0 seq length: 2000000000
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57
1 FLSELNKELEAE 1
                                                                                                                                                                                                                                                                                                                                                                                                              Match
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    BLOSUM62
Gapop 10.0 , Gapext 0.5
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLSELNKELEAE 12
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/1aa/backfiles1.pep:*
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                 В
 US-08-619-812-8
US-07-908-253-2
US-08-455-970A-2
US-08-387-156-6
US-08-694-865-6
US-08-878-748-6
US-08-124-491-6
5476657-3
US-08-455-970A-12
US-08-455-970A-10
US-08-455-970A-14
US-08-387-156-8
US-08-177-270A-8
US-08-18-8-16-4
US-08-18-7-18-9
US-08-170-18-9
US-08-170-1715-9
US-08-170-126-4
US-08-170-126-4
US-08-254-418-4
US-08-215-805A-80
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(without alignments)
9.554 Million cell updates/sec
Sequence 8, Appli
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Sequence 9, Appli
Sequence 14, Appli
Sequence 2, Appli
Sequence 20, Appli
                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                        ; MOLECULE TYPE: US-08-619-812-8
                             Query Match
Best Local 9
                 Matches
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                 Conservative
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Minimum

Sequence:

Title:

Minimum DB Maximum DB

Database

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ALIGNMENTS	US-08-940-093-119	US-08-940-093-106	US-08-940-093-75	US-08-940-095-121	US-08-940-095-119	US-08-940-095-106	US-08-940-095-75	US-08-487-459-8	US-08-432-691-8	US-08-487-461-8	US-08-288-568-8	US-07-928-930A-8	US-08-398-046-10	US-08-469-692-10	US-08-468-543-10	US-09-310-187A-1	US-08-938-105-3	US-09-045-973-7
	Sequence 119, App	Sequence 106, App		Sequence 121, App		Sequence 106, App	Sequence 75, Appl		Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 10, Appl	•	Sequence 10, Appl	Sequence 1, Appli	Sequence 3, Appli	Sequence 7, Appli

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RESULT 1
US-08-619-812-8
; Sequence 8, Application US/08619812
; Patent No. 6100066
; Patent No. 6100066
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, \
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,812
FILING DATE: 15-MAR-1996
CLASSIFICATION: 435
                                                                                          TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                               NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0019.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: POTTER, ANDREW A.
APPLICANT: THEISEN, MICHAEL
APPLICANT: HARLAND, RICHARD J.
APPLICANT: RIOUX, CLEMENT R.
TITLE OF INVENTION: VACCINES FOR HAEMOPHILUS SOMNUS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/038,719
FILING DATE: 29-MAR-1993
ATTORNEY/ACENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: REED & ROBINS
STREET: 635 BYANT STREET
CITY: PALO ALTO
STATE: CALLFORNIA
COUNTRY: UNITED STATES OF
                      TYPE: amino acid
TOPOLOGY: linear
                                                                    924 amino acids
protein
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75.4%; 75.0%;

Score 43; DB Pred. No. 15; 1; Mismatches

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Length 924; Indels

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DP 6A

424 FLININKELQAE 435

FLSELNKELEAE

12

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RESULT 2
US-07-908-253-2
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Best Local Similarity
Whiches 9; Conserv
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NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acid
                                                                                                               APPLICANT: POTTER, ANDREW A. APPLICANT: REDMOND, MARK J. APPLICANT: HUGHES, HUW P.A. TITLE OF INVENTION: ENHANCEI TITLE OF INVENTION: CHIMERA
                                                                             CORRESPONDENCE ADDRESS
                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                         424 FLLNLNKELQAE 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 199207 CLASSIFICATION: 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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          CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                            1 FLSELNKELEAE 12
                                              ADDRESSEE: REED & ROBINS STREET: 285 HAMILTON AVENUE, SUITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94301
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: UNITED STATES OF AMERICA
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635 BRYANT STREET
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UNITED STATES OF AMERICA
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PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
                                                                                                                 ENHANCED IMMUNOGENICITY USING LEUKOTOXIN CHIMERAS
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75.0%;
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          FILING DATA:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION NUMBER: US 07/779,171
APPLICATION NUMBER: US 07/779,171
TTIME DATE: 16-OCT-1991
TTIME DATE: 16-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08387156 Patent No. 5723129
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Best Local
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-0CT-1992
ATTORNBY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                          SOFTWARE: Patentin Relea
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 10-FEB-1995
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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424 FLINLNKELQAE 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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9; Conserv
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amino acid
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HUGHES, HUW P.A.
                                                                                                                                                                                                                                                                                                    UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTTER, ANDREW A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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ROBERTA L.
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75.08;
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                                                                                                                                                                   US/08/387,156
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Pred. No. 15;
1; Mismatches
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REGISTRATION NUMBER:

33,208

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; MOLECULE TYPE: protein US-08-694-865-6
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RESULT
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                                                                                                           Query Match
Best Local :
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Best Local
                                                                                              Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                   TELEFAX: (415)327-323
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                FILING DATE: 09-AUG-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: POTTER, ANDREW A. APPLICANT: MANNS, JOHN G. TITLE OF INVENTION: GORH-LEU
                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                             TELEPHONE: (415)327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 FLLNLNKELQAE 435
                                        424
                                                                                                                                                                                                                                                                                                         NAME: MCCRACKEN, THOMAS P. REGISTRATION NUMBER: 38,548 REFERENCE/DOCKET NUMBER: 90
                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94301
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/694,865
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                                                                                                                                                                                                                       LENGTH:
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                                                                 1 FLSELNKELEAE 12
                                        FLLNLNKELQAE 435
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9; Conservative
                                                                                           Similarity 75.0
9; Conservative
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amino acid
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(415)307-3231
(7) NO: 6:
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75.0%;
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                                                                                                           Score 43;
Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUITE 200
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US-08-878-748-6
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                                                                                                                                                                          Sequence 2, Application US/08535837 Patent No. 5985289
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APPLICANT: POTTER,
APPLICANT: REDMOND
APPLICANT: HUGHES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
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Best Local (
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                                                                                                                                                             GENERAL INFORMATION:
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APPLICATION NUMBER: US 01
FILING DATE: 10-FEB-1995
                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L
                                                                                           APPLICANT: POTTER, ANDREW A.
APPLICANT: HARLAND, RICHARD J.
TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 14-OCT-1992 PRIOR APPLICATION DATA:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                            424 FLLNINKELQAE 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: ROBINS, ROBERTA L REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: CALIFORNIA
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                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/779,171
                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                            1 FLSELNKELEAE 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                        Similarity 75.09; Conservative
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      2: 285 HAMILTON AVENUE, SUITE 200 PALO ALTO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       926 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUGHES, HUW P.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REDMOND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTTER, ANDREW A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327-3231
                                                                                                                                                                                                                                                                                                                                                         75.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNRH-LEUKOTOXIN CHIMERAS
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Pred. No.
                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                         Gaps
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

COUNTRY:

UNITED STATES OF AMERICA

94301

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; MOLECULE TYPE: protein US-08-535-837-2
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Best Local Similarity 75.0%;
Matches 9; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,837
FILING DATE: 27-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
                                                                     APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                               FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08
FILING DATE: 10-FEB-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/124,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: GRRH-LEUKOTOXIN CHIMERAS NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MANNS, JOHN G.
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 FLLNLNKELQAE 435
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REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0026.01
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                                                                                                                                                                                                                                          IOR APPLICATION NUMBER: US C. APPLICATION NUMBER: US C. DATE: US C. US C. US C. DATE: US C. DE C
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CITY: PALO ALTO
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APPLICATION NUMBER: US 07/779,171 FILING DATE: 16-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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Pred. No.
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15;
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RESULT 9
5476657-3
; Patent No.
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US-08-455-970A-12
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TITLE OF INVENTION: PASTEURE
COMPOSITIONS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO:3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                          Sequence 12, Application US/08455970A Patent No. 5708155
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415)327-323: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)237-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 504,850
FILING DATE: 05-APR-1990
APPLICATION NUMBER: 335,018
FILING DATE: 07-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 8
CURRENT APPLICATION LOWIBER: US/08/15,537
APPLICATION UNMBER: US/08/15,537
FILING DATE: 09-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                APPLICANT: REDMOND, MARK J. APPLICANT: HUGHES, HUW P.A. TITLE OF INVENTION: ENHANCED TITLE OF INVENTION: CHIMERAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424 FLLNLNKELQAE 435
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                              424 FLLNLNKELQAE 435
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                                               COUNTRY:
                                                                                                 STREET:
                                                                  STATE:
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                                                                                                                  ADDRESSEE:
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amino acid
DGY: linear
                                  94301
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                                                                PALO ALTO
CALIFORNIA
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(415)327-3231
- 750 TD NO: 6:
                                                                                                 285 HAMILTON AVENUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                 UNITED STATES OF AMERICA
                                                                                                                  REED & ROBINS
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75.0%;
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75.0%;
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    Mismatches

    Mismatches

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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB Pred. No. 15;
                                                                                                                                                                                   IMMUNOGENICITY USING LEUKOTOXIN
                                                                                                    SUITE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6;
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RESULT 11
US-08-455-970A-10
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
NAME: 33,208
REGISTRATION NUMBER: 30,208
REFERENCE/DOCKET NUMBER: 900
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3231
                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
TITLE OF INVENTION: CHIMERAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 327-3400
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                                                                                                                                                                                 FILING DATE: 31 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                              STREET: 285 HAM:
CITY: PALO ALTO
STATE: CALIFORNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 90
                                                                                                                                                                                              APPLICATION NUMBER: US/08/455,970A FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 75.0 les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/01 FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                             ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                CALIFORNIA
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285 HAMILTON AVENUE, SUITE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      936 amino acids
                                                                                                                                                                                                                                                                                                                                                               UNITED STATES OF AMERICA
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                         Floppy disk
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75.08;
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                                                         9001-0016.10
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Pred. No.
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Best Local Similarity /J...
Conservative
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                                                        Matches
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Best Local
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                                                                                                                                           TYPE: amino acid
TOPOLOGY: 11-
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APPLICANT:
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LENGTH: 943 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: ENHANCE
TITLE OF INVENTION: CHIMERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 327-3400
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-0CT-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33 208
REFERENCE/DOCKET NUMBER: 9001-0016
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 FILNLNKELQAE 435
424 FLININKELQAE 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: CALIFORNIA
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                                                       Conservative
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N: 424
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75.0%;
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75.0%;
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Pred. No.
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                                                        Mismatches
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RESULT

US-08-772-270A-8

Sequence 8, Patent No. (

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GENERAL INFORMATION:

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TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 956 amino
                                                                                                                                                                                                                               Sequence 8, Application US/08387156 Patent No. 5723129
                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 75.1
Matches 9; Conservative
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                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL BACTERIAL PREPARATIONS, METHOD FOR TITLE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 65
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                              APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: REED & ROBINS
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                     455 FLINLNKELQAE 466
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                                                               STREET: 635 BRYANT STREET CITY: PALO ALTO
                            COUNTRY:
                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                  1 FLSELNKELEAE 12
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40 King Street West
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Mallard, Bonnie
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                               UNITED STATES OF AMERICA
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Pred. No.
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16;
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Best Local Similarity
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REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
TELEPAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08694865 Patent No. 5837268
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 977 amino acid:
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APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-0CT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-0CT-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
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                                                                                                                         APPLICATION NUMBER: US/08/
FILING DATE: 09-AUG-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
ADDRESSEE: REED & RO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            424 FLINLNKELQAE 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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10-FEB-1995
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75.08;
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Pred. No. 16;
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Copyright (c) 1993 - 2000 Comp
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Angelos J.A., Hess J.F., George L.W.;
"Cloning and characterization of a Moraxella
Am. J. Vet. Res. 62:1222-1228(2001).
EMBL; AF205359; AAK84651.1; -.
SEQUENCE 927 AA; 98845 MW; F4B703577E10A9
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Bacteria; Proteobacteria;
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ALIGNMENTS

gamma subdivision; Moraxellaceae; Moraxella

bovis cytotoxin gene.";

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Mismatches 0;
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Pfam; PF00353; hemolysinGabind; 2.
Pfam; PF00382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 2.
SEQUENCE 1049 AA; 112308 MW; 9FA5070E48CC3127
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Bacteria; Proteobacteria;
Actinobacillus.
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Submitted (AUG-1996) to the EMBL/Genl
EMBL; U66588; AAF15370.1; -.
InterPro; IPR001343; Hemlysn_Ca_bind
InterPro; IPR003995; RtxA.
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PRINTS; PRO1488; RTXTOXINA.
PROSTITE; PSO0330; HEMOLYSIN_CALCIUM; 3.
SEQUENCE 1055 AA; 113853 MW; 5331C396FA76669E
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STRAIN-FIELD STRAIN JF1319;
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Bacteria; Proteobacteria;
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InterPro; IPR001441; UPP_synth.
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InterPro; IPR001343; Heml
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LKTA.
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003355;
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Shin S.J., Park J.Y., Choi I.S., Shin S.J., Park J.Y., Choi I for I following and Sequencing of Apx II:
"Cloning and Sequencing of Apx III:
pleuropneumoniae.";
Submitted (MAR-2001) to the EMBL/A
EMBL; APS63363; AAK50053.1;
EMBL; APS636363; AAK50053.1;
SEQUENCE 1052 AA; 112862 MW;
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01-DEC-2001
01-DEC-2001
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                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=98290540; PubMed=9628576;
Makino K., Ishii K., Yasunaga T.,
Yatsudo H.C., Kubota Y., Yamaichi
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01-JUN-2001 (TrEMBLrel.
HEMOLYSIN A (HLYA).
                                             MEDLINE=98391744;
Burland V., Shao Y
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Bacteria; Proteobacteria; gamma
 of Escherichia
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                                Blattner F.R.;
                                                                            STRAIN=EDL933;
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complete DNA sequence and analysis scherichia coli 0157:H7.";
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                                                                                                                       , Xu J., Walderhaug M.O.; (JUL-1994) to the EMBL/G
                                           Shao Y.,
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Y., Perna N.T.,
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HEMOLYSIN.
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01-OCT-2000
01-JUN-2001
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"The enterohemorrhagic Escherichia coli (EHEC)-hemolysin genes of a
Shiga toxin 1 (Stx1)- and Stx2-producing, serotype O128 Escherichia
coli strain with a greatest hemolytic activity.";
Acta Med. Blol. (Niigata) 0:0-0(2000).
EMBL; AB032930; BAA93708.1; -.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR00335; RTX_N.
Pfam; PF00382; RTX, I.
Pfam; PF00382; RTX; I.
PRINTS; PR00319; CABNDNGRPT.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 2.
SEQUENCE 998 AA; 107196 MW; CD7A88E9BD862DB6 CRC64;
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EHEC-HLYA.
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN_CALCIUM;
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EMBL; AB011549; BAA31774.1; -.
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EHEC-HLYA.
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MEDLINE-98261495; PubMed-9596716;
Boerlin P., Chen S., Colbourne J.K.,
                                                                                      Pfam; PF00353; hemolysinCabind; 2. Pfam; PF02382; RTX; 1. PRINTS; PR00313; CABNDNGRPT. PRINTS; PR01488; RTXTOXINA. PROSITE; PS00330; HEMOLYSIN_CALCIUM; SEQUENCE 998 AA; 107058 MW; OD3BE
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Pfam; PF00353; hemolysinCabind; 2.
Pfam; PF02382; RTX;
PRINTS; PR00313; CABMDNGRPT.
PRINTS; PR01486; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN_CALCIUM;
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Plasmid EHEC-hemolysin plasmid.
Bacteria; Proteobacteria; gamma subdivision;
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InterPro; IPR003995; RtxA.
InterPro; IPR003355; RTX_N.
                                                                                                                                                                                                                               Infect. Immun. 63:1055-10
EMBL; X79839; CAA56234.1;
                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
Bacteria; Proteobacteria;
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EMBL; AF043471; AAC24352.1; -.
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Q47461;
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[2]
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"Molecular analysis of the plasmid-encoded hemolysin of Escherichia
coli 0157:H7 strain Ed1933.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid p0157.
Bacteria; Proteobacteria; Escherichia.
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InterPro; IPR003995; RTxA.
InterPro; IPR003355; RTx_N.
Pfam; PF00353; hemolysinCabind; 2.
Pfam; PF02382; RTX; 1.
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"Analysis of the EHEC hly operon and its location in of the large plasmid of enterohemorrhagic Esherichia Microbiology 142:907-914(1996).

EMBL; X86087; CAA60042.1; -- Cabing
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MEDLINE=97090409; PubMed=8936317;
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Bacteria; Proteobacteria;
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Q51868; Q51866;
Q1-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-DEC-2001 (TREMBLREL. 1
LEUKOTOXIN A (FRAGMENT).
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Interpro; IPR003995; RtxA.
Interpro; IPR003355; RTX_N.
pfam; pF00353; hemolysinCabind; 2.
pfam; PF02382; RTX; 1.
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EMBL; X94129; CAA63849.1; -.
Interpro: Transcatt
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLINA. CALCIUM; 2.
SEQUENCE 998 AA; 107255 MW; DA3EF078C7E4131E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete sequence of the 1,683-kb pSymB megaplasmid fixing endosymbiont Sinorhizobium meliloti."; proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001). EMBL; AL603646; CAC49629-1; - Plasmid; Hypothetical protein; Complete proteome. SEQUENCE 387 AA; 39149 MW; 759202216369F18E CRC64;
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Finan T.M., Weidner S., Wong K., Buhr
Vorhoelter F.J., Hernandez-Lucas I.,
Golding B., Puehler A.;
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Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Sinorhizobium.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL CALCIUM BINDING PROTEIN SMB21402.
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Pred. No. 1.6;
2; Mismatches
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Pred. No.
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Last sequence update)
Last annotation updat
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Pasteurellaceae;

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RESULT
Q9EV24
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OF THE PROPERTY OF THE 
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN-T10 SEROTYPE AND T3 SEROTYPE;
Lainson A.F., Altchison K.D., Donachie W.;
Lainson A.F., Altchison K.D., Donachie W.;
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ date EMBL; Z22887; CAA80501.1; -.
EMBL; Z22887; CAA80498.1; -.
EMBL; Z22884; CAA80498.1; -.
HSSP; Q03023; IKAP.
InterPro; IPRO01343; Hemlysn_Ca_bind.
Pfam; PF00353; hemolysinCabind; 1.
PRINTS; PR00313; CABNDWGRPT.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 2.
NON_TER
1
SEQUENCE 233 AA; Z5345 MW; AD6C8408731C3F99 C
                                                                                                                                                                                                                                                                                                                                   Matches
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Q51865; Q51867;
Q10-NOV-1996 (TIEMBLIEL 01, Create
Q1-NOV-1996 (TIEMBLIEL 01, Last s
Q1-DEC-2001 (TIEMBLIEL 19, Last a
LEUKOTOXIN A (FRAGMENT).
Pasteurella haemolytica.
Bacteria; Proteobacteria; gamma su
Mannheimia.
     Q9EV24
Q9EV24;
01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001343; Hemlysn_Ca_bind pfam; pF00353; hemolysinCabind; 1. PRINTS; PR00313; CABNDNGRPT. PROSITE; PS00330; HEMOLYSIN_CALCIUM; NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lainson A.F., Altchison K.D., Donachie W.; Submitted (JUN-1993) to the EMBL/GenBank/DDBJ EMBL; 222885; CAA80499.1; -. EMBL; 22886; CAA80500.1; -. EMBL; 22886; CAA80500.1; -.
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NCBI_TaxID=75985;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasteurella haemolytica.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=75985;
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nes 7; Conserv
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  (TrEMBLrel. (TrEMBLrel.
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                                                                                                      PRELIMINARY;
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58.3%;
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Last sequence update)
Last annotation updat
Created)
Last sequence update)
Last annotation update)
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AD6C8408731C3F99 CRC64;
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1.3;
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J. Bacteriol. 183:1394-1404(2001).

J. Bacteriol. 183:1394-1404(2001).

R EMBL; AP314521; AAG40305.1; .

R InterPro; IPR001753; Enoyl_CoA_hydrtse.

R InterPro; IPR001343; Hemlysn_Ca_bind.

R InterPro; IPR003355; RTX_N.

R Pfam; PF00353; hemolysinCabind; 1.

R Pfam; PF00352; RTX; 1.

R Pfam; PF00313; CABUDUGRPT.

R PRINTS; PR00313; CABUDUGRPT.

R PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.

SEQUENCE 946 AA; 101480 MW; 25C077858BDC76C4 CRC64;
                                                                       Query Match
Best Local
                                                                                                                                                                    "Sequence diversity and molecular evolution of the 1 gene in bovine and ovine strains of Mannheimia (Past haemolytica.";

J. Bacteriol. 0:0-0(2001).

EMBL; AF314518; AAG40302.1; -.

EMBL; AF314517; AAG40302.1; -.

REMBL; AF314517; AAG40301.1; -.

InterPro; IPR001753; Encyl_coA_hydrtse.

InterPro; IPR001343; Hemlysn_Ca_bind.

InterPro; IPR003343; Hemlysn_Ca_bind.

InterPro; IPR00335; RTX_N.

Pfam; PF00353; hemolysinCabind; 1.

Pfam; PF00382; RTX; 1.

Pfam; PF00382; RTX; 1.

PFANTY; PR00313; CABNDUGRPT.

REMOSITE; PS00166; ENCYL_COA_HYDRATASE; UNKNOWN_1.

PROSITE; PS00166; ENCYL_COA_HYDRATASE; UNKNOWN_1.
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Best Local
                                                   Matches
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Q9ETX2;
Q1-MAR-2001
01-MAR-2001
01-JUN-2001
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"Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA)
Gene in Boyine and Ovine Strains of Mannheimia (Pasteurella)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mannheimia.
NCBI_TaxID=85401;
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-PH498, AND PH344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Mannheimia.
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     2 NDIFHSGEGDDL
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                                                Similarity 7; Conserv
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7; Conserv
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                                                     Conservative
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                                                                          63.6%;
58.3%;
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58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S., Selander R.K.;
molecular evolution of
e strains of Mannheimia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma
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Pred. No. 6.4;
3; Mismatches
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Last annotation updat
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                                                                          Score 49; I
Pred. No. 6
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                                           core 49; DB:
red. No. 6.5;
Mismatches
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update)

Pasteurellaceae;

(Pasteurella)

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Length 946

Indels

0

Gaps

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2;

Length 953

Indels

0

Gaps

0;

CRC64;

Db 774 NDLLHGGKGDDI 785

Search completed: September 11, 2002, 09:01:27 Job time: 285 sec

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Minimum DB
Maximum DB
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No.
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
   seq length: 0 seq length: 2000000000
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	1 CAPA_CAEEL 1 ALF_CAMJE 1 JI60_HORVU 1 JI60_HORVU 1 METX_YEAST 1 CLPE_LACLC 1 FRPA_NEIMC 1 FRPA_NEIMB 1 TKTC_METJA 1 LON_MYCGE 1 PLON_MYCGE 1 PODA_MOUSE 1 NODA_MOUSE 1 SYS_PYRAB
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	p34685 p53818 000531 004533 Q94533 Q9s5z2 p55126 Q9k0k9 Q9k092 Q9k092 P4747 P4747 P4747 P4747

ALIGNMENTS

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: M27399; AAA21922.1; B34345; B34345. ; P04002; 1WFA. ; P070; 1PR001343; Hemlysn_Ca_bind.	to stra	DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY). PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN MODIFIED (BY SIMILARITY). DISEASE: ITS TARGET CELL SPECIFICITY IS RESTRICTED TO HUMAN AND SOME NON-HUMAN CELLS OF THE MONOMYELOCYTIC LINEAGE. SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.		"Analysis of the Actinobacillus actinomycetemcomitans leukotoxin gene. Delineation of unique features and comparison to homologous toxins."; 1. Biol. Chem. 264:15451-15456(1999). 1. FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.ACTINOMYCETEMCOMITANS MIGHT BE A CYTOTOXIN, POSSIBLY THE MEMBRANE-BOUND HEMOLYSIN.	NCBI_TaxID=714; [1] SEQUENCE FROM N.A. STRAIN=JP2; STRAIN=B9359382; PubMed=2670940; MEDLINE=89359382; PubMed=2670940; Lally E.T., Golub E.E., Kieba I.R., Taichman N.S., Rosenbloom J., Lally E.T., Golub C.W., Demuth D.R.;	actinomyceto mitans). obacteria;	ACTAC ACTAC EKTALACTAC STANDARD; PRT; 1050 AA. P16462; PRT; 1050 AA.

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Best Local
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01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                   MEDLINE=93263992; PubMed=8494611; Chang Y.-F., Shi J., Ma D.-P., Shin S.J., "Molecular analysis of the Actinobacillus toxin-III gene cluster."; DNA Cell Biol. 12:351-362(1993).
                                                                                                                                                                                                                                                                                                                                                                  ACTPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01488; I
PROSITE; PS00330;
                                                                    operons: characterization of the ApxIII operons: Infect. Immun. 62:4411-4418(1994).
-!- FUNCTION: DOES NOT HAVE HEMOLYTIC ACTIVITY
                                                                                                                             SEQUENCE OF 828-1049 FROM N.A. STRAIN=1536 / SEROTYPE 2; MEDLINE=95012630; PubMed=7927703;
                                                                                                                                                                                                                                                                                              RTX-III toxin determinant A from serotype 2 IIIA) (CLY-IIIA).
                                                                                                           Jansen R.,
Smits M.A.
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-SEROTYPE 2;
                                                                                                                                                                                                                                                               Actinobacillus pleuropneumoniae (Haemophilus Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                     APXIIIA OR CLYIIIA OR RTXA OR PTXA
                                                                                                                                                                                                                                               NCBI_TaxID=715;
                                                                                                  "Genetic map of the Actinobacillus
                                                                                                                                                                                                                                                         Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                       734
                                                                                                                                                                                                                                                                                                                                                                                                                          μ
    CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-E
ACTIVITY (BY SIMILARITY).
DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE
INVOLVED IN PORE FORMATION BY THE CYTOTOXIN
                                       CYTOTOXICITY TOWARDS ALVEOLAR MACROPHAGES SUBCELLULAR LOCATION: Secreted.
DOMAIN: THE GLY-RICH REGION IS PROBABLY IN
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Cytolysis; Cytotox:
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Pred. No. 0.032;
3; Mismatches
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                                                                                                                     A.B.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38DF9AA24649F662 CRC64;
                                                                                            pleuropneumoniae
pxIII operons.";
                                           PROBABLY INVOLVED
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                                                                                          operons.
                                                                                                                      Kamp
                               LY INVOLVED IN BINDING CELL-BINDING OR CYTOL
                                                                                                                                                                                                  Lein D.H.;
                                                                                                                                                                                       pleuropneumoniae
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                                                                                                                                                                                                                                                                                                           (APX-IIIA)
                                                                                                                                                                                                                                                                   pleuropneumoniae)
Pasteurellaceae;
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     (BY
               BELIEVED TO
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    IEVED TO BE SIMILARITY).
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REPEAT
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InterPro; IPRO03355;
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Toxin; Cytolysis; Cytotoxin; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00353; hemolysinCabind;
pfam; PF02382; RTX; 1.
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01-OCT-1996
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                                                                         Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Actinobacillus.
ACBI_TaxID=715;
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operons:
                    Smits M.A.;
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                                     STRAIN=405 / SEROTYPE MEDLINE=95012630; Pubb
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        "Genetic map of the Actinobacillus pleuropneumoniae
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Rel. 39, Last annotation update)
determinant A from serotype 8 (
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           TYPE 8;

PubMed=7927703;

e J., van Geel A.B.M., Kamp E.M., Gielkens A.L.J.,
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                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                        (Haemophilus
   ApxIII
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                                                                                                                                                                                  1052 AA

 Calcium;

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  operons.";
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                                                                                                                                    (APX-IIIA) (Cytolysin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage
                                                                                                         pleuropneumoniae).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
                                                                                                                                                                                                                                                                                      Length 1049
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MBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Infect. Immun. 61947-954(1993).

-I- FUNCTION: DOES NOT HAVE HEMOLYTIC ACTIVITY BUT SHOWS A STRONG CYTOTOXICITY TOWARDS ALVECLAR MACROPHAGES AND NEUTROPHILS.
-I- SUBCELLULAR LOCATION: Secreted.
-I- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYT ACTIVITY (BY SIMILARITY).

-I- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
-I- PTM: PALMITOXILATED BY APXIIIC. THE TOXIN ONLY BECOMES ACTIVE
HLYA_ECOLI STANDARD;
P08715;
01-JAN-1988 (Rel. 06, Created)
                                                                                                                                                                                                                     REPEAT
REPEAT
                                       _ECOLI
                                                                                                                                                                                                                                                                                                                                                                               Lipoprotein;
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00313; CABNDNGRPT PRINTS; PR01488; RTXTOXINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00353; hemolysinCabind; Pfam; PF02382; RTX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00330; HEMOLYSIN_CALCIUM;
Toxin; Cytolysis; Cytotoxin; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and characterization of the Actinobacillus pleuropneumoniae-RTX-toxin III (ApxIII) gene.";
                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
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SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                     FRDIFHGADGDDLL
                                                                                                            FNDIFHSGEGDDLL
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X68815; CAA48711.1;
                                                                                                                                    Similarity
10; Conserv
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IPR003995; RtxA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162836; PubMed-8432615;
Briaire J., Kamp E.M.,
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Pred. No. 0.047;
1; Mismatches
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                                                                                                                                                                                               F83AFE25A6FD8758 CRC64;
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                          1024
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Calcium;
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                          AA
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                                                                                                                                                          Length 1052;
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   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                         DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stanley P., Packman L.C., Koronakis V., Hughes C.; "Fatty acylation of two internal lysine residues required for the toxic activity of Escherichia coli hemolysin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1988 (Rel. 01-MAR-2002 (Rel.
                                                                                   TRANSMEM
                                                                                             PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4. Repeat; Calcium; Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium; Transmembrane; Lipoprotein; Palmitate; Plasmid.
                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                  This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PALMITOYLATION OF LYS-564 AND LYS-690 MEDLINE=95099325; PubMed=7801126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                            TRANSMEM
                                                                                                                                   PRINTS; PR00313; CABNDNGRP PRINTS; PR01488; RTXTOXINA
                                                                                                                                                            Pfam;
                                                                                                                                                                                                                      EMBL; M14107; AAA98233.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PALMITOYLATION OF LYS-564 AND LYS-690
MEDLINE-96404790; PubMed-8808931;
Ludwig A., Garcia F., Bauer S., Jarch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEMS Microbiol.
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                                                                                                                                                                                InterPro; IPR003995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science
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SEQUENCE FROM N.A.

Nucleotide sequence of a plasmid-encoded hemolysin determinant and its comparison with a corresponding chromosomal hemolysin sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriol. 178:5422-5430(1996).
- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
                                                                                                                                                                                                                                                                                                                                                                    MODIFIED.
- DISEASE: 7
STRAINS CA
                                                                                                                                                                                                                                                                                                                                                                                                                               CALCIUM,
ACTIVITY.
DOMAIN: T
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                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN PALMITOYLATED BY HLYC. THE TOXIN ONLY I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                        {
m SWISS-PROT} entry is copyright. It is produced through a collaboration een the {
m Swiss} Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                            PF02382; RTX;
                                                                                                                                                                      PF00353; hemolysinCabind;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266:1992-1996(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid
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Last annotation updat
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POTENTIAL.
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                                                 REPEATS,
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                                                 GLY-RICH
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P16535;
01-AUG-1990
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                                                                                                                                                                                                                          "Nucleotide sequence of the leukotoxin haemolytica Al.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                          Highlander S.K., Engler M.J., Weinstock G.M.;
"Secretion and expression of the Pasteurella haer
J. Bacteriol 172:2343-2350(1990).
-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS
CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECI
                                                                                                                   SEQUENCE OF 884-953 FROM N.A. STRAIN=SEROTYPE A1 / PHL101; MEDLINE=90236888; PubMed=2185213;
                                                                                                                                                                     MEDLINE-89210283; PubMed-2707120;
Highlander S.K., Chidambaram M., Engler M.J., Weinstock
"DNA sequence of the Pasteurella haemolytica leukotoxin
                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
STRAIN-SEROTYPE A1 / PHL101;
                                                                                                                                                                                                                                                                                                                                       01-AUG-1990
30-MAY-2000
                                                                                                                                                                                                                                                               STRAIN=SEROTYPE A1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIPID
                                                                                                                                                        DNA 8:15-28(1989).
                                                                                                                                                                cluster
                                                                                                                                                                                                                                                        MEDLINE=87306837; PubMed=3040588;
                                                                                                                                                                                                                                                                                       NCBI_TaxID=75985;
                                                                                                                                                                                                                                                                                                Mannheimia
                                                                                                                                                                                                                                                                                                        Bacteria;
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                                                                                                                                                                                                                                                                                                                Pasteurella haemolytica
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    PTM: PALA
                                           SUBCELLULAR LOCATION: Secreted DOMAIN: THE GLY-RICH REGION IS CALCIUM, WHICH IS REQUIRED FOR
                ACTIVITY.

DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN ONLY F
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   PALMITOYLATED
FIED (BY SIMILA
                                                                                                                                                                                                                                                                                                        Proteobacteria;
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(Rel. 15, Last seq
(Rel. 39, Last ann
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                                            PROBABLY INVOLVED TARGET CELL-BINDIN
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[13
             TOXIN ONLY
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                                            CELL-BINDING OR CYTOL
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                                                                             MECHANISMS NOT CLEARLY
                                                                                                      haemolytica Leukotoxin.";
                                                                                                                                                                                                                                         of Pasteurella
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             BECOMES
                    (BY SIMILARITY)
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             ACTIVE
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                                                                                                                                                                                 G.M.;
                                             CYTOLYTIC
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RESULT 6
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                         STRAIN-SERVILLE 94041617; PubMed-0222.
MEDLINE-94041617; PubMed-0222.
BUTTOWS L.L., Olah-Winfield E., Lo R.Y.C
"Molecular analysis of the leukotoxin de
"Molecular analysis of the 10 16.";
haemolytica scrotypes 1 to 16.";
haemolytica scrotypes 1 to 193).
LI Infect. Immun. 61:5001-5007 (1993).
LI Infect. Immun. 61:5001-5007 (1993).
LI INFORMATION: BACTERIAL HEMOLYSINS ARE
- STINCTION: BACTERIAL HEMOLYSINS ARE
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HSSP; P02392; 1CTF.
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01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00313; CABNDNGRPF
PRINTS; PR01488; RTXTOXINA
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Pfam; PF00353; hemolysinCabind;
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                                                                                                                                                                                                                                                                                                                                               01-OCT-1996
30-MAY-2000
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                                                                                                                                               SEQUENCE FROM N.A.;
STRAIN-SEROTYPE All;
MEDLINE-94041617; Pub. Med. 225575;
                                                                                                                                                                                                                                                                   Bacteria;
                                                                                                                                                                                                                                                                                                             LKTA
                                                                                                                                                                                                                                                   Mannheimia
                                                                                                                                                                                                                                                                                         Pasteurella
                                                                                                                                                                                                                                                                                                                               Leukotoxin
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SUBCELLULAR LOCATION:
                   DEFINED
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58.3%;
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D -> Y (IN REF. 2).
V; 7F93D113A118C05F
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                                                                                                                                                                                                                                                                       subdivision;
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                                     S ARE EXOTOXINS THAT ATTACK BLOOD RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                 on update)
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                                                                                                                 (.C.;
determinants
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RESULT 7
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1D P55117
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DT 01-OCT
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DT 01-OCT
DT 01-OCT
CO LEUKOT
GN LKTA.
OS PASTEU
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RP SEQUE
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Matches 7
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P55117;
01-OCT-1996
01-OCT-1996
30-MAY-2000
SEQUENCE FROM N.A.

STRAIN-SEROTYPE T10;

MEDLINE-96425875; PubMed-8828217;

MEDLINE-96425875; PubMed-8828217;

Lainson F.A., Murray J., Davies R.C., Donachie W.;

"Characterization of epitopes involved in the neutralization of Pasteurella haemolytica serotype Al leukotoxin.";

Microbiology 142:2499-2507(1996).

-1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
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Pfam; PF02382; RTX; 1.
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DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO HE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).

THE TOXIN ONLY BECOMES ACTIVE WHEN
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SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY
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                                                                                                                                                                                                                                                                                           haemolytica
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39, Last annotation update)
erotype T10.
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58.3%;
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6 X REPEATS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                    subdivision; Pasteurellaceae;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; L
Transmem 299
Transmem 361
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DOMAIN 736
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SEQUENCE 955 A
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between
SEQUENCE FROM N.A.
STRAIN-S 4074 / SEROTYPE 1;
MEDLINE-91348845; PubMed-1879928;
Frey J., Meier R., Gygi D., Nicol.
"Nucleotide sequence of the hemol
pleuropneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTPL
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InterPro; IPR003355; RTX_N.
InterPro; IPR003355; RTX_N.
Pfam; PF00353; hemolysinCabind; 1.
pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
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                                                                                                                                                                       Actinobacillus.
NCBI_TaxID=715;
                                                                                                                                                                                                                    Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae) Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4. Hemolysis; Toxin; Cytolysis; Cytotoxin;
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DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOL
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European Bioinformatics Institute.
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Pred. No. 1.4;
3; Mismatches
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6 X REPEATS,
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SEQUENCE
STRAIN=S
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Chang Y., Wang Y., Chin N.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
-i- EUNCTION: ONE OF THE VIRULENCE FACTORS OF A.PLEUROPP
WHICH HAS A STRONG HEMOLYTIC ACTIVITY AND IS CYTOTO
ALYEOLAR MACROPHAGES AND NEUTROPHILS.
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"Structural analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ISOLATE CVI 13261 / SEROTYPE MEDLINE-93366425; PubMed-8359891;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 142:97-102(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frey J., Haldimann A., Nicolet J., Boffini A., Prentki P.; "Sequence analysis and transcription of the apxI operon (hemolysin from Actinobacillus pleuropneumoniae.";
                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                    InterPro; IPR001343; Hemlysn_Ca_bind InterPro; IPR003355; RTX_N. InterPro; IPR003995; RtxA.
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8, 12, AND TOTALLY DELETED IN SEROTYPE 3.
MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF SEROTYPE 1.
SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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DOMAIN: THE GLY-RICH REGION IS
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x73117;
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CAA51548.1;
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                                                                                                                                                                                                                                                              STRAIN=K17 / SEROTYPE 5;
MEDLINE=96401417; PubMed=8807793;
Chin N., Frey J., Chang C.F., Chang 'Identification of a locus involved: Actinobacillus pleuropneumoniae.";
FEMS Microbiol. Lett. 143:1-6(1996).
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01-OCT-1996
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MEDLINE=94276858; PubMed=8007819;
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P55129;
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Jansen R., Briaire J., Kamp E.M., Gielkens
"Structural analysis of the Actinobacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Actinobacillus.
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Bacteria; Proteobacteria; gamma
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                                                                                                                                                                       Infect.
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GCT. IMMUN. 61:3688-3695(1993).

WHICH HAS A STRONG HEMOLYTIC ACTIVITY AND IS CYTOTOXIC FOR ALVEOLAR MACROPHAGES AND NEUTROPHILS.

SUBCELLULAR LOCATION: Secreted.

SUBCELLULAR LOCATION: SPROBABLY INVOLVED IN BINDING; DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING; CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
MISCELLANEOUS: APXIA IS PARTIALLY DELETED IN SEROTYPES 8, 12, AND TOTALLY DELETED IN SEROTYPE 3.
MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF SEROTYPE SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMIL
                                             DOMAIN: THE THREE TRANSMEMBRANE D
INVOLVED IN PORE FORMATION BY THE
PTM: PALMITOYLATED BY APXIC: THE
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                                                                                                     CALCIUM, WHICH IS REQUIRED
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Pred. No.
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R -> A (IN REF. 3 AND 4).
Q -> E (IN REF. 3 AND 4).
TC -> R (IN REF. 3 AND 4).
TC -> R (IN REF. 3 AND 4).
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   RTX PROKARYOTIC TOXIN FAMILY.
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                                                                      THE
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in the
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Pasteurellaceae;
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BECOMES ACTIVE
                                      SEROTYPES
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Best Local Similarity
Matches 8; Conser
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P09983;
01-MAR-1989
01-MAR-1989
30-MAY-2000
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SEQUENCE
SEQUENCE FROM N.A.
STRAIN-J96 / SEROTYPE 04;
MEDLINE-85234404; Pubmed-3891743;
Felmlee T., Pellett S., Welch R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
TRANSMEM
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InterPro;
InterPro;
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Bacteria; P
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REPEAT
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Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 2.
Hemolysis; Toxin; Cytolysis; Cytotoxin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                      Hemolysin,
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between the Swiss Institute of Bioinformatics and the EMBL
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U04954;
X73116;
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                                                             Proteobacteria;
                                                                                       chromosomal.
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(Rel. 10, Last sequence update)
(Rel. 39, Last annotation update)
                                                                      coli
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26 256
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3 AA;
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E -> Q (IN REF. 2).
TC -> R (IN REF. 2).
F -> L (IN REF. 2).
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                                                             subdivision; Enterobacteriaceae;
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    Q (IN REF. 2).
    > R (IN REF. 2).
    L (IN REF. 2).
    183C7C15EE57DB55 CRC64;

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PALMITATE (BY SIMILARITY).

REPEAT

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InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
InterPro; IPR003355; RtxA.
Pfam; PF00353; hemolysinCabind; 2.
Pfam; PF02382; RTX; 1.
                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Nucleotide sequence of an Escherichia coli chromosomal hemolysin.";
J. Bacteriol. 163:94-105(1985).
[2]
SEQUENCE OF 1-44 FROM N.A.
                                                                                                                                REPEAT
REPEAT
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REPEAT
REPEAT
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                                                                                                                                                                                                                                               Transmembrane;
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DISEASE: THE HEMOLYSIN OF E.COLI IS PRODUCED PREDOMINANTLY STRAINS CAUSING EXTRAINTESTINAL INFECTIONS, SUCH AS THOSE CURINARY TRACT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted.
DOMAIN: THE GLY-RICH REGION IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL MEMBRANES AND CAUSE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                          326
410
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737
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POTENTIAL.
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POTENTIAL.
16 X REPEA
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SEQUENCE FROM N.A., AND SEQUENCE OF 4-18.

SEQUENCE FROM N.A., AND SEQUENCE OF 4-18.

MEDILING-90078125; PubMed=2887250;
de Maagd R.A., Mijfies A.H.M. Spaink H.P., Ruiz-Sainz J.E.,

Wijffelman C.A., Okker R.J.H., Lugtenberg B.J.J.;

Mijffelman C.A., Okker R.J.H., Lugtenberg B.J.J.;

ModO, a new nod gene of the Rhizobium leguminosarum biovar viciae sym plasmid pRLJuI, encodes a secreted protein.";

J. Bacteriol. 171:6764-6770(1989).

1- FUNCTION: THE NODO PROTEIN MAY PLAY A ROLE IN NODULE DEVELOPMENT BY DIRECT INTERACTION WITH THE ROOT HALR CELLS OR SOME OTHER PLAN SURFACE IN A. CA(2+)-DEPENDENT MANNER.

SURFACE IN A. CA(2+)-DEPENDENT MANNER.

SURFACE IN A. CA(2+)-DEPENDENT MANNER.

TINUOLYDE AN N-TERMINAL SIGNAL PEPTIDE.

TINUOLYDE AN N-TERMINAL SIGNAL PEPTIDE.

TINUOLYDE AN N-TERMINAL SIGNAL PEPTIDE.

TO THE PLAN SECRETED BY A MECHANISM THAT DOES NOT INVOLVE AN N-TERMINAL SIGNAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NODO_RHILV
P15728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The Rhizobium nodulation W.D.O., Johnston A.W.B., Downie J.A.;
"The Rhizobium nodulation gene nodO encodes a Ca2(+)-binding protein that is exported without N-terminal cleavage and is homologous to haemolysin and related proteins.";
EMBO.T 0.340-367-37000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NODO OR NOLR
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                                                                                                                                                                PROSITE; Plasmid;
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EMBL; M29532; AAA2634
PIR; S08385; S08385.
PIR; A43721; A43721.
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                                                                                                                                                                                            PRINTS; PR00313; CABNDNGRPT PROSITE; PS00330; HEMOLYSIN_
        SEQUENCE
                                                                                                             DOMAIN
                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                          InterPro; IPR001343; Hemlysn_Ca_bind
InterPro; IPR003355; RTX_N.
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                                                                                                                                                                                                                                                 PF00353; hemolysinCabind; 2.
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8; Conser
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        284
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                                                                                                                                                                                              HEMOLYSIN_CALCIUM; 1.
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           9CA41DCFCBDF8E15 CRC64
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2.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Å
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TRANSMEM

Transmembrane; Lipoprotein; Hemolysis; Toxin; Cytolysis;

PROSITE; PS00330;

PRINTS; PRINTS;

PR01488; RTXTOXINA

HEMOLYSIN_CALCIUM;

cytotoxin; Palmitate.

Repeat; Calcium;

POTENTIAL.
9 X REPEAT

REPEATS,

GLY-RICH

POTENTIAL POTENTIAL PR00313;

CABNDNGRPT.

InterPro; IPR003995; RtxA.
pfam; PF00353; hemolysinCabind;
pfam; PF02382; RTX; 1.

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Matches 8
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01-APR-1993 (Rel. 25, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
Hemolysin (Cytolysin II) (CLY-IIA) (HLY-IIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage humor sequires a license agreement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPA OR CLYTIA OR HLYIIA OR CYTC. Actinobacillus suis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92267623;
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                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001343; InterPro; IPR003355;
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M90440; AAA21918.1;
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P15377;
01-APR-1990
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REPEAT
SEQUENCE
             InterPro;
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                                                PIR;
                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang Y.-F., Young R., Struck D.K.; "Cloning and characterization of a hemolysin gene (Haemophilus) pleuropneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-SEROTYPE 5;
MEDLINE-90126233; PubMed-2693022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinobacillus pleuropneumoniae Bacteria; Proteobacteria; gamma Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
RTX-II toxin determinant A (APX-IIA) (Hemol
                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                           entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                         Gielkens A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-ISOLATE CVI 13261 / SEROTYPE MEDLINE-92040145; PubMed-1937809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Cytolysin IIA) (CLY-IIA).
APXIIA OR CLYIIA OR HLYIIA OR APPA OR CYTC.
                                                                                    EMBL; M30602;
                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                      Smits M.A., Briaire
                                                                                                                                                                                                                                                                                                                                                                Infect.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=715;
                                                                                                                                                                                                                                                                                                                                                                Cytolysins of Actinobacillus pleuropneumoniae serotype 9.", Infect. Immun. 59:4497-4504(1991).
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SUBCELULAR LOCATION: Secreted.

DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN STREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).

PTM: PALMITOYLATED BY AFXIIC. THE TOXIN ONLY BECOMES ACTIVE
                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                            FUNCTION: ONE OF THE VIRULENCE FACTORS OF WHICH SHOWS A WEAK HEMOLYTIC ACTIVITY AND FOR ALVEOLAR MACROPHAGES AND NEUTROPHILS.
                                                B33389; B33389.
S18853; S18853.
                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration seen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                            MODIFIED (BY SIMILARITY).
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                                                                                                                                                                         the Swiss Institute of Bioinformatics
           IPR001343; Hemlysn_Ca_bind IPR003355; RTX_N. IPR003995; RtxA.
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956
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 hemolysinCabind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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SEQUENCE
                                                                                           use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                EMBL; L12148; AAA16444.1;
                                                                                                                                                                                                                        the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 morecular characterization of a leukotoxin gene haemolytica-like organism, encoding a new member family ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chang Y.-F., Ma D.-P., Shi J., Chengappa M.M., "Molecular characterization of a leukotoxin ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasteurella haemolytica-like sp. (strain 5943B).
Bacteria; Proteobacteria; gamma subdivision; Pas
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DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY). PTM: PALMITOYLATED BY LATC. THE TOXIN ONLY BECOMES ACTIVE WHEN MODIFIED (BY SIMILARITY).

SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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FUNCTION: VIRULENCE FACTOR WHICH
IS NOT HEMOLYTIC.
                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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RA Wassif C., Cheek D., Belas R.;
RY "Molecular analysis of a metalloprotease from Proteus mirabilis.";
RI "Molecular analysis of a metalloprotease from Proteus mirabilis.";
RL J. Bacteriol. 177.5790-5798 (1995).
GC CILL DIFFERENTIATION OF THE BACTERIA, WHICH SEEMS TO BE ASSOCIATED COCK.
GELL DIFFERENTIATION OF THE BACTERIA, WHICH SEEMS TO BE ASSOCIATED COCK.
GC IG A2, AS WELL AS IG DEGRADATION.
GC IG A2, AS WELL AS IG DEGRADATION.
GC I- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
GC I- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
GC I- ENZYME REGULATION: CA2+ INCREASES PROTEASE ACTIVITY.
G- I- SUBCELLULAR LOCATION: Secreted.
G- I- SUBCELLULAR ECCRETION OF THIS METALLOPROTEASE.
G- I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10B (ZINC METALLOPROTEASE); ALSO KNOWN AS THE SERRALYSIN SUBFAMILY.
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01-0CT-1996 (Rel. 34, Last annotation update)
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InterPro; IPR003995;
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                                              use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BB2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
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154 170 POTENTIAL.
312 33 POTENTIAL.
393 414 POTENTIAL.
25 780 7 X REPEATS, G
30 74 3.
19 744 3.
19 753 4.
17 762 5.
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RtxA.
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Pred. No. 6.9;
4; Mismatches
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7 X REPEATS, GLY-RICH
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                                                                               (See http://www.isb-sib.ch/announce/
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AAA86729.1;

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Best Local 9
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MEROPS; M10.057; ...

InterPro; IPR001343; Hemlysn_Ca_bind.

InterPro; IPR00130; Zn_MTpeptdse.

Pfam; PF00353; hemolysinCabind; 1.

PRINTS; PR00313; CABMONGRPT.

SMART; SM00235; ZnMC; 1.
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347 NDIIHGNDADNTLIGGEGDDII 368
                 2 NDIFH-----
                                l Similarity
9; Conserv
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                 -SGEGDDLL 14
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Pred. No. 8.
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BY SIMILARITY.
                                                                                                                                                               EXTRACELLULAR METALLOPROTEASE ZINC (CATALYTIC) (BY SIMILARIT
                                                                                                                               ZINC
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Search completed: September 11, job time: 278 sec 2002, 09:01:55

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Result
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Maximum DB seq length: 2000000000
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            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
               PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd
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hypothetical prote probable secreted probable outer mem conserved hypothet probable protein k hypothetical prote iron-regulated procalcium-binding pr
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toxin III - Actino
hemolysin A - Esch
hemolysin - Escher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
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ALIGNMENTS

A; Residues: 430-438, 'S', 440-476, 'R', 478-506, 'RVRS', 511, 'QSIAINSLNTD', 523-541, 'I', 543, A; Note: this sequence is revised in reference A34345 R; Ohta, H.; Miyagi, A.; Kato, K.; Fukul, K. submitted to JIPID, July 1995 A; Description: Modulation of leukotoxin production by growth rate and bicarbonate in A; Reference number: PH0266 A; Accession: PH0267 A; Molecule type: protein A; Residues: 17-42 < OHT> A; Residues: 17-42 < OHT> A; Experimental source: strain 301-b A; Accession: PH0266	A; Molecule type: DNA A; Residues: 1-239,'Y',241-259,'H',261-335,'A',337-415,'S',417-438,'S',440-723,'N',725 A; Residues: 1-239,'Y',241-259,'H',261-335,'A',337-415,'S',417-438,'S',440-723,'N',725 A; Cross-references: GB:M27933 A; Cross-references: GB:M27933 A; Lally, E.T.; Kieba, I.R.; Demuth, D.R.; Rosenbloom, J.; Golub, E.E.; Taichman, N.S Biochem. Biophys. Res. Commun. 159, 256-262, 1989 A; Title: Identification and expression of the Actinobacillus actinomycetemcomitans le A; Reference number: A32276; MUID:89165863 A; Accession: A32276 A; Status: nucleic acid sequence not shown; not compared with conceptual translation A; Molecule type: DNA	A;Note: the authors present evidence that the nucleotide sequence is correct in the vising nucleotide R;Kolodrubetz, D.; Dailey, T.; Ebersole, J.; Kraig, E. Infect. Immun. 57, 1465-1469, 1989 A;Title: Cloning and expression of the leukotoxin gene from Actinobacillus actinomyc- A;Reference number: A60768; MUID:89212893 A;Accession: A60768 A;Accession: A60768 A;Residus: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: DNA A;Residues: 297-309, 'Y', 311-364;434-440, 'KC', 443-474, 'H', 476-489, 'S', 491-493, 'VLK', 49 A;Note: this sequence is revised in reference A37205 R;Lally, E.T.; Golub, E.E.; Kieba, I.R.; Taichman, N.S.; Rosenbloom, J.; Rosenbloom, J. Biol. Chem. 264, 15451-15456, 1989 A;Title: Analysis of the Actinobacillus actinomycetemcomitans leukotoxin gene. Deline A;Reference number: A34345 A;Accession: B34345	nomycete

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A; Molecule type: protein
A; Residues: 2-6, 'L', 8-26 <OH2>
C: Genetics:
A; Gene: ltxA
C; Function:
A; Description: lyses human polymorphonuclear lymphocytes and monocytes
C; Superfamily: hemolysin A; hemolysin A homology
C; Keywords: cytolysis; hemolysis; lipoprotein; periplasmic space; tande
F; 731-847/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F; 552,687/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                            toxin III - Actinobacillus pleuropneumoniae (serotype 8)
N;Alternate names: RTX-toxin III (ApxIIIA)
C;Species: Actinobacillus pleuropneumoniae
C;Date: 19-Dec-1993 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
C;Accession: B49219; S48043; S29958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-1049 <CHA>
A; Cross-references: EMBL:L12145; NID:g349605; PIDN:AAA21924.1;
C; Comment: This orgnism causes porcine pleuropneumonia.
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: S51784
R;Chang, Y.F; Shi, J; Ma, D.P.; Shin, S.J.; Lein, D.H.
DNA Cell Biol. 12, 351-362, 1993
A;Title: Molecular analysis of the Actinobacillus pleuropneumoniae
A;Reference number: S51783; MUID:93263992
A;Accession: S51784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: apxIIIA
C;Function:
A;Description: lyses lung macrophages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: RTX-toxin IIIA (ApxIIIA, C;Species: Actinobacillus pleuropneumoniae C;Date: 14-Jul-1995 #sequence_revision 15-
A; Molecule type: DNA
A; Residues: 1-1052 < JAN1>
                                    A; Title: Cloning and characterization of the A; Reference number: A49219; MUID:93162836 A; Accession: B49219
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                                                                                                 Infect.
                                                                                                                R; Jansen,
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Best Local Similarity
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                                                                                           n, R.; Briaire, J.; Kamp, E.M.; Gielkens, A.L.; Immun. 61, 947-954, 1993
                                                                                                                                                                                                                                                                                                                                         FNDIFHSGEGDDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinobacillus pleuropneumoniae names: RTX-toxin IIIA (ApxIIIA)
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9; Conserv
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64.3%;
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71.4%;
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Pred. No. 0.088;
3; Mismatches
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                           Actinobacillus pleuropneumoniae-RTX-toxin
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hemolysin - Escherichia coli C;Species: Escherichia coli C;Date: 31-May-1996 #sequence_revision 31-May-1996 C;Accession: I41078

#text_change

21-Jul-2000

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A;Title: Nucleotide sequence of a plasmid-encoded A;Reference number: S07209
A;Accession: S10056
A;Status: prolitical pro
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A;Accession: $48043
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A; Note: sequence extracted from NCBI backbone (NCBIN:125168, NCBIP:125170)
R; Jansen, R.; Briaire, J.; van Geel, A.B.M.; Kamp, E.M.; Gielkens, A.L.J.;
Infect. Immun. 62, 4411-4418, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Comment: This orgnism causes porcine pleuropneumonia. C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: hemolysir C; Keywords: lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Escherichia coli
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997
C;Accession: S10056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: lyses lung macrophages
C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: calcium binding; cytolysis; exotoxin
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A;Experimental source: strain 405, serotype 8
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Ju
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                                                                                                                                                                                                                                                                                                                                                                                                                              F; 247-792/Domain: F; 564, 690/Binding
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C;Superfamily: hemolysin A; hemolysin A homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-1024 <HES>
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RESULT
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A;Residues: 1-1052 <JAN2>
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Best Local
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9; Conser
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71.4%;
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Pred. No. 0.13
1; Mismatches
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DNA Res. 5, 1-9, 1998

A)Title: Complete nucleotide sequences of
A)Title: Complete 114127; MUID:98290540
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A;Accession: I41078
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-998 <RES>
                                                                                                                                                                                                                                                                                                                                                                    A;Genome: plasmid pO157
C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: cytolysis; hemolysis; lipoprotein; to
E;233-776/Domain: hemolysin A homology <HLYA>
F;550,675/Binding site: palmitate (Lys) (covalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Status: preliminary; translated from GB/EMBL/DDB
A:Molecule type: DNA
A:Residues: 1-998 <BUR>
A:Cross-references: EMBL:AF074613; PIDN:AAC70116.1
A:Experimental source: strain EDL933; serotype O15
C:Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hemolysin A toxin protein - Escherichia coli plasmid p0157 C;Speciles: Escherichia coli C;Speciles: Escherichia coli C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000 C;Accession: T00227; T42148 R;Makino, K.; Ishii, K.; Yasunaga, T.; Hattori, M.; Yokoyama, K.; Yatsudo, R;Makino, K.; Ishii, K.; Yasunaga, T.;
hypothetical protein all2655 C; Species: Anabaena sp.
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A; Residues: 1-998 <MAK>
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                                                                                                                                                                                                                                                    Matches
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Best Local :
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                                                                                                                                                                                                                                               Similarity
8; Conserv
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57.1%;
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57.1%;
                      [imported]
                                                                                                                                                                                                                                                                      Score 52;
Pred. No. 1
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Pred. No. 1.3;
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1.3;
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leukotoxin A - Pasteurella haemolytica (fragment) N;Alternate names: lktA protein C;Species: Pasteurella haemolytica C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 C;Accession: S34238; S34236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AL591985; PIDN:CAC49629.1; PID:g15141116; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 568-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: E95995
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,883-kb pSymB megaplasmid
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: E95995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C;Accession: AH2137 R;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriqu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabatz DNA Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Heference number: AB1807; MUID:21595285; PMID:11759840
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S34238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical calcium binding protein [imported] - Sinorhizobium meliloti (strain C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: E95995
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A; Residues: 1-387 <KUR>
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9; Conserv
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69.2%;
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69.2%;
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Pred. No. 0.
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06-Jan-1995 #text_change

23-Mar-2001

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A; Description: lyses leukocytes C; Superfamily: hemolysin A; hemolysin A homology C; Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipo E; 238-784/Domain: hemolysin A homology <HLYA> F; 716-807/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X) F; 554/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-741,'D',743-953 <LOR>
A;Residues: 1-741,'D',743-953 <LOR>
A;Cross-references: EMBL:M20730; NID:g150492; PIDN:AAA25529.1; PID:g150494
C;Comment: This organism causes bovine pneumonic pasteurellosis (shipping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-953 <HIG>
R;Strathdee, C.A.; Lo, R.Y.C.
J. Bacteriol. 171, 91-6-82, 1989
A;Title: Cloning, nucleotide sequence, and A;Reference number: A32051; MUID:89123172
A;Accession: C32051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Pasteurella haemolytica
C;Date: 12-Oct-1989 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
C;Accession: B30169; C32051; S29516
R;Highlander, S.C.; Chidambaram, M.; Engler, M.J.; Weinstock, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: lktA
C;Species: Pasteurella h
C;Date: 12-Oct-1989 #seq
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                                                                                                                                                                                C; Function:
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                                                                                                                                                                                                                                C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                         R;Lo, R.Y.C.; Strathdee, C.A.; She Infect. Immun. 55, 1987-1996, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 947-953 <STR>
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A; Residues: 9-208 <LA2>
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A; Experimental source: serotype
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A; Residues: 1-208 <LAI>
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A; Accession: S34238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
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58.3%;
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T4
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Pred. No. 0.74
3; Mismatches
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C; Function: attacks cell membranes and causes coll specific time.

A; Description: attacks cell membranes and causes collision as hemolysin A homology
C; Superfamily: hemolysin A; hemolysis; exotoxin; hemolysis; lipor; Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipor; 240-786/Domain: hemolysin A homology <HIYA>
F; 240-786/Domain: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 950-955 <HIG>
A;Cross-references: GB:M24197; GB:M34943; GB:M34944
R;Lainson, A.F.; Aitchison, K.D.; Donachie, W.
submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 745-955 <LA2>
A;Cross-references: EMBL:Z22884; NID:g311828; PIDN:CAA80498.1;
A;Experimental source: serotype T3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, September 1993 A; Description: DNA sequence of the leukotoxin A gen A; Reference number: S37145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: lktA protein C;Species: Pasteurella haemolytica C;Species: Pasteurella haemolytica C;Date: 10-Aug-1990 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999 C;Accession: S37145; A35254; S34237; S34235 R;Lainson, A.F.; Aitchison, K.; Donachie, W.
                                                                                                                                                                                                                                                                                                                                                F;718-809/Region: F;718-726/Region:
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A; Residues: 723-955 <LA3>
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A; Residues: 1-955 <LAI>
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                                        Matches
                                                         Query Match
Best Local
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776

NDLLHGGKGDDI

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A; Molecule type: DNA
A; Residues: 604-685 <TAS>
A; Residues: 604-685 <TAS>
C; Comment: This organism causes porcine pleuropneumonia.
C; Genetics:
A; Genetics:
C; Superfunction: attacks blood cell membranes and causes cell lysis
C; Superfamily: hemolysin A; hemolysin A homology
C; Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipo;
F; 721-847/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F; 7560,686/Binding site: palmitate (Lys) (covalent) #status predict
Infect. Immun. 61, 3688-3695, 1993
A.Title: Structural analysis of the Actinobacillus pleuropneumoniae-RTX-toxin I (ApxI)
A;Reference number: I39641; MUID:93366425
A;Accession: I39643
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A; Residues: 1-209, 'AMPYLTLA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022 <RE2>
A; Cross-references: EMBL: X68595; NID: g505568; PIDN: CAAA48586.1; PID: g505570
A; Cross-references: EMBL: X68595; NID: g505568; PIDN: CAAA48586.1; PID: g505570
R; Tascon, R.I.; Vazquez-Boland, J.A.; Gutierrez-Martin, C.B.; Rodriguez-Barbosa,
Mol. Microbiol. 14, 207-216, 1994
Mol. Microbiol. 14, 207-216, 1994
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A;Rosidues: 1-209, 'AMPYLTLA', 218-373,'R', 375-561,'Q', 563-686,'TC', 688-1022
A;Cross-references: EMBL:X52899; NID:g38949; PIDN:CAA37081.1; PID:g38950
R;Frey, J.; Haldimann, A.; Nicolet, J.; Boffini, A.; Prentki, P.
Gene 142, 97-102, 1994
A;Title: Sequence analysis and transcription of the apxI operon (hemolysin A;Reference number: I39644; MUID:94237497
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C;Speciles: Actinobacillus pleuropneumoniae
C;Speciles: Actinobacillus pleuropneumoniae
C;Date: 19-Jul-1996 #sequence_revision 08-Nov-1996 #text_change 18-Jun-1999
C;Accession: I39643; S18769; I39645; S60732; S35781
R;Jansen, R.; Briaire, J.; Kamp, E.M.; Gielkens, A.L.; Smits, M.A.
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A;Accession: S60732
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Infect. Immun. 59, 3026-3032, 1991
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1; Mismatches
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  O.; Nelson, K.E.; Ketchum, K.A.; D; Sutton, G.G.; Gill, S.; Kirkness,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hemolysis; lipoprotein;
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A; Description: attacks blood cell membranes and causes cell lysi: C; Superfamily: hemolysin A; hemolysin A homology C; Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lip: F; 246-791/Domain: hemolysin A homology <HLYA> F; 723-851/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X) F; 563,689/Binding site: palmitate (Lys) (covalent) #status exper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Title: Fatty acylation of two internal lysine residues required A.Reference number: A55387; MUID:95099325
A.Contents: annotation; lysine palmitoylation
A.Note: lysine modification is performed by the hlyC gene product R:Haertlein, M.; Schiessl, S.; Wagner, W.; Rdest, U.; Kreft, J.; G. J. (Cell Biol. 22, 87-97, 1983
A.Title: Transport of hemolysin by Escherichia coli.
A.Reference number: I41280
A.Accession: I41280
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A; Residues: 1-1023 <FEL>
A; Cross-references: GB:M10133; GB:M12863; NID:g146377;
A; Experimental source: strain J96, O4 serotype
R; Stanley, P.; Packman, L.C.; Koronakis, V.; Hughes, C.
Science 266, 1992-1996, 1994
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J. Bacteriol. 103, 94-105, 1985
A;Title: Nucleotide sequence of an Escherichia
A; Reference number: A24433; MUID:85234404
A; Accession: A24433
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A; Residues: 1,'T',3,'V',5,'T',7-44 <RES>
A; Cross-references: GB: M29173; NID: g146337; PIDN: AAA23957.1;
                                                                                                                                                                                                                                                                                                              C; Function
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A; Residues: 1-334 <KLE>
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Nature 390, 364-370, 1997
                                                                  Query Match
Best Local
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69.2%;
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                                                                    62.3%;
66.7%;
                                              Score 48; DB Pred. No. 6.3; Nismatches
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Pred. No. 1.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN:AAA23975.1; PID:g146379
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                                                                                                                                                                                                                                                                                                                                                                                   PID:g146338
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hypothetical protein all7655 [imported] - Anabaena sp. (strain PCC 7120) plasmid pCC7120 C.Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C.Accession: AD2546 R.Raneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriquchi Raneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriquchi Raneko, T.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. 201-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anala, Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD2546
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-302 <KUR>
A;Cross-references: GB:AP003602; PIDN:BAB77298.1; PID:g17134740; GSPDB:GN00181
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: al17655
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AD2546
                                                                                                                                                                                                                                                                                                                                                                                                               A;Genome: plasmid
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Search completed: September 11, 2002, 09:00:14 Job time: 232 sec
                                                                                                                                                                                                                                                                Query Match 61.0%;
Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                  3 DIFHSGEGDDLL 14
|||| | ||||
85 DIFHRGGADDLL 96
                                                                                                                                                                                                                                                                      Score 47; DB 2; Length 302; Pred. No. 2.4; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                  0;
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Sequence Patent No. Sequence Sequence Sequence

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2, Appli 8, Appli 2, Appli 2, Appli 2, Appli 4, Appli 4, Appli 10, Appli 10, Appli 10, Appli 11, Appli 11, Appli 11, Appli 12, Appli 13, Appli 15, Appli 15, Appli 15, Appli 16, Appli 17, Appli 18, Appli 19, Appli 19, Appli 19, Appli 11, Appli 11, Appli 11, Appli 11, Appli 12, Appli 13, Appli 14, Appli

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OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB seq length: DB seq length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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77
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11.146 Million cell updates/sec
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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PCT-US93-10500-2
US-08-258-188-2
US-08-526-813-2
PCT-US95-08554-2
US-08-6526-813-2
PCT-US95-08554-2
US-08-455-970A-2
US-08-387-156-6
US-08-878-748-6
US-08-878-7491-6
S47657-3
US-08-455-970A-12
US-08-455-970A-12
US-08-455-970A-14
US-08-455-970A-14
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US-08-455-970A-14
US-08-455-970A-14
US-08-877-775-9
US-08-877-775-9
US-08-954-418-4
US-08-954-418-4
US-08-954-418-4
US-08-954-418-4
US-08-954-418-4
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       sequence 6, App.
Sequence 2, Appl.
Sequence 2, Appl.
Sequence 12, Appl.
Sequence 12, Appl.
Sequence 10, Appl.
Sequence 10, Appl.
Sequence 14, Appl.
Sequence 8, Appl.
sequence 8, Appl.
quence 8, Appl.
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ce 4, Appl.
ence 9, Appl.
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                                                                                        ; MOLECULE TYPE: Protein
; ORIGINAL SOURCE:
; ORGANISM: Actinobacillus
US-08-772-270A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
US-08-772-270A-11
                                                                                                                                          TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1049 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
Query Match
Best Local Similarity /1...
Best Local Similarity /1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Applicat Patent No. 6019984 GENERAL INFORMATION:
                                                                                                                                                                                                                                         ATTORNEY, AND THE MICHELINE NAME: Gravelle, Micheline REGISTRATION NUMBER: 40,261 REFERENCE/DOCKET NUMBER: 6580 TELECOMMUNICATION INFORMATION: 7ELEPHONE: (416) 364-7311
                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/772,270A
FILING DATE: December 23, 1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MacInnes, Janet
APPLICANT: Ricciatti, Paul
APPLICANT: Mallard, Bonnie
APPLICANT: Rosendal, Soren
TITLE OF INVENTION: NOVEL BACTERIAL PREPARATIONS, METHOD FOR
TITLE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin & Parr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 40 Kin
CITY: Toronto
STATE: Ontario
COUNTRY: Canad
ZIP: M5H 3Y2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canada
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71.4%;
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US-09-609-124A-10

US-09-120-440B-10

US-09-173-492-10

US-09-173-133-10

US-07-745-206A-15

US-08-311-363-15

US-08-311-363-13

US-08-311-363-13
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US-08-772-270A-8
US-08-215-805A-80
US-08-669-785-2
5183745-6
                   Score 58; DB Pred. No. 0.11
1; Mismatches
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US-08-387-942C-3
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                                   DB 3;
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Length 1049; Indels

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Searched:

Scoring table:

Post-processing:

Title: Perfect score:

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                                                                US-08-258-188-2
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APPLICANT: Chang, Yung-Fu
             Sequence 2, Application US/08258188 Patent No. 5475098 GENERAL INFORMATION:
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: KORMAN, Alan S.
REGISTRATION NUMBER: 133,932
REFERENCE/DOCKET NUMBER: 196(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-853-8104
TELEFAX: 716-853-8109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 716-853-8109
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1244 amino acid
TYPE: amino acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07 FILING DATE: 05-NOV-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE:
                                                                                                                                920 FRDIFHGADGDDLL 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                 ORGANISM: Actinobacillus p
STRAIN: Serotypes 2, 3, 4,
INDIVIDUAL ISOLATE: Swine
CELL TYPE: Gram negative k
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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                                                                                                                                                               1 FNDIFHSGEGDDLL 14
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                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                 Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                   : peptide
NO
                                                                                                                                                                                                                                                                                                 Gram negative bacterium
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 Robert H.
                                                                                                                                                                                                                 75.3%;
71.4%;
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                                                                                                                                                                                                                 Score 58; DB 5
Pred. No. 0.13;
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                                                                                                                                                                                                                                 DB 5;
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RESULT 4
US-08-526-813-2
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                          PATENTE OF INVENTION: A New and Distinctive DNA Sequence of E. PATENT NO. 5756293
PATENTE OF INVENTION: coli 0157:H7 and its Use for the Rapid, TITLE OF INVENTION: Specific Detection of 0157:H7 and Other TITLE OF INVENTION: E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08526813 Patent No. 5756293 GENERAL INFORMATION:
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Best Local
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TITLE OF INVENTION: A
TITLE OF INVENTION: C
TITLE OF INVENTION: S
TITLE OF INVENTION: E
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NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330

REGISTRATION NUMBER: 17,28020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 14-JUN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                     STATE:
                                                                                                                                                                                         CITY: San Francisco
                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
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                                                                                                                                             COUNTRY:
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8; Conserv
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) 543-5043
) ID NO: 2:
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                                                                                                                                                                                                                                                                        coli O157:H7 and its Use for the Rapid, Sensitive and Specific Detection of O157:H7 and Other Enterohemorrhagic E. coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.5%;
57.1%;
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US/08/526,813

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PCT-US95-08554-2
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                                                                                TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
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                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 758 amino acids
                                                                                                  TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-9643
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPUTER: PC DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION UNMERE. DATA:
ABBITCATION NUMBER. DCT/(1605/0855)
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TITLE OF INVENTION: A NI
TITLE OF INVENTION: COLI
TITLE OF INVENTION: SPEC
TITLE OF INVENTION: E.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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FILING DATE: 14-JUN-1994
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
MOLECULE TYPE: protein
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                    TOPOLOGY:
                                                                                                                                                         NAME: Garrett-Wackowski, Eu REGISTRATION NUMBER: 37,330 REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US95/08554 FILING DATE: 14-JUN-1994 CLASSIFICATION:
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                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A NEW AND DISTINGTIVE DNA SEQUENCE OF E. COLI O157:H7 AND ITS USE FOR THE RAPID, SENSITIVE AND SPECIFIC DETECTION OF O157:H7 AND OTHER ENTEROHEMORRHAGIC E. coli
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57.1%;
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                                                                                                                                                         15280206, DHHSE135940
                                                                                                                                                                                           Eugenia
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Pred. No. 0.75;
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                                                                                                                                                                                                                                                                                                     #1.25
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RESULT 7
US-07-908-253-2
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US-08-619-812-8
                                                       Sequence 2, Application US/07908253 Patent No. 5534256
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                       Query Match
Best Local
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ZIP: 94301
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: 15M PC compatible
TOMPHTER: TEM PC-DOS/MS-DOS
TOPHTER: TOMPHTER: PC-DOS/MS-DOS
                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 29-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICANT: POTTER, ANDREW A. APPLICANT: HARLAND, RICHARD J. TITLE OF INVENTION: HAEMOPHILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                               747 NDLLHGGKGDDI 758
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REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                                                                         Similarity 7; Conserv
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HARLAND, RICHARD J.
RIOUX, CLEMENT R.
TVENTION.
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                                                                                                                                                                                                            Conservative
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HAEMOPHILUS SOMNUS OUTER MEMBRANE
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57.1%;
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Pred. No. 0.75;
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Pred. No. 2.
                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                         Gaps
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PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS

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Best Local Similarity
7; Conserva
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CITY: PALO ALTO
CTATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                STREET: 200 CITY: PALO ALTO
CITY: CALIFORNIA
CTATE: CALIFORNIA
                                                                                                                                                                                                                                                                                              APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
TITLE OF INVENTION: CHIMERAS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein -908-253-2
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NUMBER OF SEQUENCES:
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                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 14-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       747 NDLLHGGKGDDI 758
                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Pc-10--
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TELEFAX:
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FILING DATE: 19920702
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OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 33,208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                           APPLICATION NUMBER: US/08/455,970A FILING DATE: 31-MAY-1995
                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 NDIFHSGEGDDL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : (415) 617-8999
(415) 327-3231
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                                                                                                                                                                                                                UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                    POTTER, ANDREW A.
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58.3%;
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            US 07/960,932
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Pred. No.
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2.9;
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-387-156-6
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
ETILING DATE: 16-OCT-1991
ATTORNEY_AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                                             TELEFAX: (415) 327-3231 INFORMATION FOR SEQ ID NO: 6:
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CORRESPONDENCE ADDRESS:
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APPLICANT: REDMOND,
APPLICANT: HUGHES, H
                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
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                                                                             SEQUENCE CHARACTERISTICS:
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| 747 NDLLHGGKGDDI 758
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                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                            REGISTRATION NUMBER:
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                                                             LENGTH:
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                                              amino acid
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                                                               926 amino acids
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HUGHES, HUW P.A.
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                               linear
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Pred. No. 2.9;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-694-865-6
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Best Local Similarity
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US-08-878-748-6
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                                                                                                                                                        Sequence 6, Application US/08878748 Patent No. 5969126
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Best Local
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                                            GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: GORH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, VG
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/694,865
FILING DATE: 09-AUG-1996
CLASSIFICATION: 424
ACCOUNTY ACCOUNT TANGEMENTS.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
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NAME: MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
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CORRESPONDENCE ADDRESS: BEETING TIP
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CITY: PALO ALTO
STATE: CA
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285 HAMILTON AVENUE, SUITE 200
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58.3%;
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Pred. No. 2.9;
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                 Mismatches
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2.9;
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RESULT 12
US-08-535-837-2
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Best Local
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOBTICE DOBTER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
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LENGTH: 926 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                 ADDRESSEE: ROBERTA L.
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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FILING DATE: 27-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      747 NDLLHGGKGDDI 758
                                                                                                                                                                                                                STREET: 285 HAMILTON AVENUE, CITY: PALO ALTO STATE: CALIFORNIA COUNTRY. HATCHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: ROBINS, ROBERTA L. REGISTRATION NUMBER: 33,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA
                                                      APPLICATION NUMBER: FILING DATE: 27-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 7; Conserv
                                                                                                                                                                                                  94301
                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08535837
                                                                                                                                                                                                               UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                       HARLAND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                           POTTER, ANDREW A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUN-1997
                                                                                                                                                                                                                                                                                                                                      HAEMOPHILUS SOMNUS OUTER MEMBRANE
PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.6%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                            RICHARD J.
                                                                     US/08/535,837
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; TOPOLOGY: 1; MOLECULE TYPE: , US-09-124-491-6
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; Sequence 6, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 327-323
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,865
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
APPLICATION NUMBER: US 07/779,171
APPLICATION LORGE: 16-OCT-1991
                                                                                                                          TELEFAX: (415)327-3231 (NFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 900
REFERENCE/DOCKET NUMBER: 900
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: POTTER, ANDREW A. APPLICANT: MANNS, JOHN G. TITLE OF INVENTION: GNRH-LEU
                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acid
                                                                                                                                                                                                                     FILLING FACENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
                                                                                                                                                               REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
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TYPE: amino acid
TOPOLOGY: linear
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                                                              amino acid
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                                                                                926 amino acids
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                                                                                                                                                                                                           9001-0016.22
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2.9;
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RESULT 1, 5476657-3
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Best Local Similarity
"hes 7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: POTTER, ANDREW A.
TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA LEUKOTOXIN; COMPOSITIONS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 07-APR-1989 SEQ ID NO:3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1. Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 09-FEB-1993
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                           APPLICATION NUMBER: US/08/455,970J
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: POTTER, ANDREW J.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: ENHANCE
TITLE OF INVENTION: CHIMERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                           CITY: PALO ALTO
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o. 5708155
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                                                                                                                                                                                                                                                                                           285 HAMILTON AVENUE,
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                                                                                                                                                                                                                                           UNITED
                                                                                                                                                                                                                                                                                                          REED & ROBINS
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CHIMERAS
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58.3%;
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Pred. No. 2.
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REGISTRATION NUMBER:

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REFERENCE/OCKET NUMBERS: 9001-0015.10

TELECHOME: (415) 327-3400

TELECHOME: (415) 327-3201

LENDOMATION FOR SEQ LD NO: 12:
SEQUENCE CHARACTERISTICS:
TPPE: Minito Sciid
TPPE: Minito Minito Sciid
TPPE: Mi
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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HLYA_SERMA
RBP1_PLAVB
HLYA_PROMI
NODO_RHILV
SLAP_BACST
SLAP_CAUCR
PWPD_CHLMU
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pfam; PF00353; hemolysinCabind;
Pfam; PF02382; RTX; 1.
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EMBL; M24197; AAA25543.1;
PIR; S29516; S29516.
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                                       GAPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYA
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                                                                                  AYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDG
                                                                                                                                                                                   HANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAV
                                                                                                                                                                                                                    GFELANQVVGNITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFN
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INRYDSWKITDGAASSTFDLTNVVQRIGIELDNAGNVTKTKETKIIAKLGEGDDNVFVGS
                   FGRVKNWQVTDGEASSKLDFSKVIQRV-----
                                                                                                                               ASPIALLVSGITGVISTILQYSKQAMFEHVANKIHNKIVEWEKNNHGKNYFENGYDARYL
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6 X REPEATS, GLY-RICH (BY SI
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                    AETEGTDEIGLIVNAKAGNDDIFVGQ
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P55118;
01-OCT-1996
01-OCT-1996
                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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                     InterPro;
InterPro;
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MEDLINE-94041617; PubMed-8225575;
Burrows L.L., Olah-Winfield E., I
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Bacteria; Proteobacteria;
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                                                                    InterPro;
                                                                                               EMBL; U01215;
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DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY) PM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE W MODIFIED (BY SIMILARITY).
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                        215; AAB36689.1; -.
IPR001343; Hemlysn_Ca_bind.
IPR003355; RTX_N.
IPR003995; RtxA.
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                                                                      TVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQ
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RESULT 3

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DT 01-OCT
CR PASTEU
OC Bacteu
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LKTA_PASSP
P55123;
01-OCT-1996
01-OCT-1996
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TRANSMEM
DOMAIN
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SEQUENCE FROM N.A.
MEDIINE=93239320; PubMed=8478098;
Chang Y.-F., Ma D.-P., Shi J., Chengappa M.M.;
"Molecular characterization of a leukotoxin gene"
"Molecular characterization of a new member
                                                                                                                                               PRINTS; PRO0313; C
PRINTS; PRO1488; F
PROSITE; PS00330;
                                                                                                                                                                                                       Pfam; PF00353; hemolysinCabind; Pfam; PF02382; RTX; 1.
                                                                                                                                                                                                                                          EMBL; L12148; AAA16444.1; -... InterPro; IPR001343; Hemlysn_Ca_bind. InterPro; IPR003355; RTX_N. InterPro; IPR003995; RtxA.
                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pasteurella haemolytica-like sp. Bacteria; Proteobacteria; gamma
                                                                             TRANSMEM
                                                                                               TRANSMEM
                                                                                                                  Transmembrane;
                                                                                                                                  Hemolysis; Toxin; Cytolysis;
                                                                                                                                                                                                                                                                                                                                                                            modified
                                                                                                                                                                                                                                                                                                                                                                                                                                   between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY) PTM: PALMITOYLATED BY LATC. THE TOXIN ONLY BECOMES ACTIVE W MODIFIED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Secreted.

DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING (
                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE RTX PROKARYOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IS NOT HEMOLYTIC
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39,
                                                                                                                                                   HEMOLYSIN_CALCIUM;
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Last sequence Last anno
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                                                                                                            Cytotoxin; Palmitate.
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 DENKSQKLSASDIAS-SLNKLVGSMALFGTAN
                        FREADYAKTVHNYQAT-ADEKIEEIIGRQGERITSKQIDELIEKGKG--KIDQSELERIA
                                     GNDILCTVKG-GNDSISDSGGNDRLSFADSNLKDLTFEKVNHHLMI-TNVKKEKVTIQNW
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Pred. No. 1.8e-111;
3; Mismatches 252;
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01-OCT-1996
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94041617; PubMed=8225575;
Burrows L.L., LO R.Y.C., Olah-Winfield
"Molecular analysis of the leukotoxin d
haemolytica serotypes 1 to 16.";
Infect. Immun. 61:5001-5007(1993).
Infect. Immun. 61:5001-5007(1993).
REPEAT
REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-SEROTYPE T3;
                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                           modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                             between
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                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                      ACTIVITY.

DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORWATION BY THE CYTOTOXIN (BY SIMILARITY) PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE W MODIFIED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted.
DOMAIN: THE GLY-RICH REGION IS
CALCIUM, WHICH IS REQUIRED FOR
                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY
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                                                                                                                                                                                                      IPR003995; RtxA
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IPR003355; RTX_N.
                                                                                                                                   Toxin;
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(Rel. 34, Last sequence up
(Rel. 39, Last annotation
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Query Match Best Local Similarity

48.6%; 48.7%;

Score Pred.

2256; No. 1

DB 1; .1e-108

Length

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RT2A_ACTPL
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                                                                                                   YQLLKYS-RDASNSLDKLISSASAFTSSND-SRNVL---ASPT-SMLDPSL
                                                                                                                                                                                                               DVYIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWY-
                                                                                                                                                                                                                                                                  KGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGN
                                                                                                                                                                                                                                                                                                   VESGKALHEVTSTHTALVGNREEKIEYR-HSNNQHHAGYYTKDTLKAVEELIGTSHNDIF
                                                                                                                                                                                                                                                                                                                  VARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQENDVF
                                                                                                                                                                                                                                                                                                                                                                    GLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRK
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|||:|||:|||:|||:|||:|||:|||
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                                                                                                                                                                                                                                                                                                                                                                                                                             SRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVA-----ETEGTDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNGGKNYFENGYDARYLANLQDNMKFLLNLNKELQAERVIAITQQQWDSNIGDLAGISRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALAISPLSFAGIADKFDRAKSLENYAERFKKLGYEGDSLLAEYQHGTGTIDASVTAINTA
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                                                                                                                         NKSQKLSASDIASSLNKLVGSMALFGTANSVSSNALQPITQPTQGILAPSV
                                                                                                                                                                                                   DIFVHRQGDGNDSITESEGNDKLSFSDSNLKDLTFEKVNHHLVI-TNTKQEKVTIQNWFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAAIAGGVSAAAAGSVVASPIALLVSGITGVISTILQYSKQAMFEHVANKIHNKIVEWEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGN
                                                                                                                                                                                                                                                     KGSKFNDAFNGGDGVDTIDGNDGNDRLFGGKGDDIIDGGNGDDFIDGGKGNHLLHGGKGV
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 14,
14,
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             Created)
 sequence
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              SEQUENCE FROM N.A.
STRAIN=SEROTYPE 5;
MEDLINE=90126233; PubMed=2693022;
Chang Y.-F., Young R., Struck D.K.;
"Cloning and characterization of a her (Haemophilus) pleuropneumoniae.";
DNA 8:635-647(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Z | SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=ISOLATE CVI 13261 / SEROTYPE
MEDLINE=92040145; PubMed=1937809;
MEDLINE=92040145; PubMed=1937809;
MEDLINE=92040145; PubMed=1937809;
                                                                                                                          TRANSMEM
DOMAIN
                                                                                                                                                                                                              InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
InterPro; IPR003355; RTX_N.
Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Actinobacillus. NCBI_TaxID=715;
                                     REPEAT
REPEAT
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REPEAT
                                                                                                                                                                                                                                                                                                   EMBL; M30602; AAA87232.1;
EMBL; X61111; CAA43423.1;
PIR; B33389; B33389.
PIR; S18853; S18853.
                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                       REPEAT
                                                                                                                                                               TRANSMEM
                                                                                                                                                                                      PROSITE; PS00330; HEMOLYSIN_CALCIUM; Hemolysis; Toxin; Cytolysis; Cytotox:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cytolysins of Actinobacillus pleuropneumoniae
Infect. Immun. 59:4497-4504(1991).
-!- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gielkens A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Cytolysin IIA) (CLY-IIA).
APXIIA OR CLYIIA OR HLYIIA OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Last annotation update) RTX-II toxin determinant A (APX-IIA) (Hemolys
                                                                                                                                                                            Transmembrane; Lipoprotein;
                                                                                                                                                    CRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted.

DOMAIN: THE GLY-RICH REGION IS PROBABLY CALCIUM, WHICH IS REQUIRED FOR TARGET CE ACTIVITY (BY SIMILARITY).

DOMAIN: THE THREE TRANSMEMBRANE DOMAINS INVOLVED IN PORE FORMATION BY THE CYTOTC PM: PALMITOYLATED BY APXIIC. THE TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MODIFIED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: ONE OF THE VIRULENCE FACTORS OF WHICH SHOWS A WEAK HEMOLYTIC ACTIVITY AND FOR ALVEOLAR MACROPHAGES AND NEUTROPHILS.
                                     233
266
361
361
719
719
728
737
746
755
                                     256
323
406
787
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751
769
7789
              102531
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                      POTENTIAL.
POTENTIAL.
8 x REPEATS
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4.
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6.
7.
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                                                                                                                                                                                      CALCIUM; 1.
Cytotoxin;
                                                                                                                                                               POTENTIAL.
             BDBCABBADF14A641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROBABLY INVOLVED IN TARGET CELL-BINDING
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                                                                                                                                                                                         Repeat;
                                                                                                                           GLY-RICH
                                                                                                                                                                                                                                                                                                                                                                            http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pleuropneumoniae)
Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                          Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kamp
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              CRC64;
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSKITLSSLKSSLQQGLKNGKNKLNQAGTTLKNGLTQTGHSLQNGAKKLILYIPQGYDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMALFGTANSVSSN 910
                                                                                                                                                                                                     DGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVK
                                                                                                                                                                                                                                                                 KSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLL
                                                                                                                                                                                                                                                                                                                           GTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYQSTDNL
                                                                                                                                                                                                                                                                                                                                                                   DDAGNIIESKDTK---IIANLGAGNDNVFVGSSTTVIDGGDGHDRVHYSR-GEYGALVID
                                                                                                                                                                                                                                                                                                                                                                                                                           LFRTPLLTPGEENRERIQEGKNSYITKLHIQRVDSWTVTDGDASSSVDFTNVVQRTAVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWD 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGLELTNELVGNIASSVQTVDAFAEQISKLGSHLQNVKGLGGLSNKLQNLPDLGKASLGL
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                                                                      NNQISAEALSKVVNDYNTSK-DRONVSNSLAKLISSVGSFTSSSDFRNN
                                                                                                                                                                                                                                                                                                          ATAETEKGSYSYKRYVGDSKALHETIATHQTNVGNREEKIEYR-REDDRFHTGYTVTDSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIDASVTTINTALAAISGGVGAASAGSLVGAPVALLVAGVTGLITTILEYSKQAMFEHVA
                                                                                                                                                                                         VGGTGNDIISGGKDNDIYVHKTGDGNDSITDSGGQDKLAFSDVNLKDLTFKKVDSSLEI-
                                                                                                                                                                                                                                                 KSVEEIIGSQFNDIFKGSQFDDVFHGGNGVDTIDGNDGDDHLFGGAGDDVIDGGNGNNFL
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47.8%;
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Pred. No. 7e-108;
88; Mismatches 254;
                                                                   935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
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LKAA_PASHA

STANDARD;

PRT;

955 AΑ

> δã В Qγ

49 12 G

NGIRSTLTATRGGLNRAGQSLTQAGQTLKNGAKKIILYIPKDYKYDSGSGNGLQDLVKAA Matches Query Match Best Local

Similarity

48.1%; 48.2%; 178;

Score 2236; DB 1; Pred. No. 1.2e-107; 8; Mismatches 271;

Length

Indels

44;

17;

Conservative

---STKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAA

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U1-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
Leukotoxin from serotype T10.
LKTA.
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01-OCT-1996
01-OCT-1996
30-MAY-2000
                                        TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 110;
STRAIN-SEROTYPE 110;
MEDLINE-96425875; PubMed-8828217;
MEDLINE-96425875; PubMed-8828217;
Medline-96425875; PubMed-8828217;
REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                              InterPro; IPR003995; RtxA.
Pfam; PF00353; hemolysinCabind;
Pfam; PF02382; RTX; 1.
                                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microbiology 142:2499-2507(1996).
-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lainson F.A., Murray J., Davies R.C., Donachie W. "Characterization of epitopes involved in the neu Pasteurella haemolytica serotype Al leukotoxin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
Mannheimia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=75985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pasteurella haemolytica.
                             REPEAT
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                                                                                                                                     TRANSMEM
                                                                                                                                                Transmembrane;
                                                                                                                                                            PROSITE; PS00330; HEMOLYSIN_(Hemolysis; Toxin; Cytolysis;
                                                                                                                                                                                        PRINTS;
                                                                                                                                                                                                    PRINTS;
                                                                                                                                                                                                                                                     InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
                                                                                                                                                                                                                                                                                EMBL; Z26247; CAA81206.1;
                                                                                                                                                                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY) PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE W MODIFIED (BY SIMILARITY).

SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted.

DOMAIN: THE GLY-RICH REGION IS PROBABI
CALCIUM, WHICH IS REQUIRED FOR TARGET
                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                      PR00313; CABNDNGRPT. PR01488; RTXTOXINA.
                                                                                                                                                Lipoprotein;
                                                                                                                                                                          HEMOLYSIN_CALCIUM;
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  MW;
                                                                                                                                                Cytotoxin;
Palmitate.
                                                                                           POTENTIAL.
6 X REPEAT
                                                                                                                     POTENTIAL.
POTENTIAL.
               55.48.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subdivision;
  B60F2DB8168EBCAF
                                                                                            REPEATS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Donachie W.;
d in the neutralization
                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                              There are no restrictions
                                                                                                                                                            Repeat; Calcium;
                                                                                            GLY-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pasteurellaceae;
  CRC64;
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OR CYTOLYTIC
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                                                              HLYA_ACTSU STANDARD; PRT; 956 AA. 000951; 01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) 40-MAY-2000 (Rel. 39, Last annotation (CYC-IIA) (CYA-IIA) (
  Actinobacillus.
NCBI_TaxID=716;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=3714;
                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00353; hemolysinCabind;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M90440; AAA21918.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92267623; PubMed=1587585;
                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecular characterization of
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DOMAIN: THE GLY-RICH REGION IS
CALCIUM, WHICH IS REQUIRED FOR
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                                                                                         KGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQ
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                                                                                                                                           MSNINV--IKSNIQAGL---------NSTKSGLKNLYLAIPKDYDPQ
           ASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNL-NFSKTNLGL
                                       KNP--KIGNTLGSASSISQNIGKANTVLGGIQSILGSVLSGVNLNELLQNKDPNQLELAK
                                                         KHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAK
                                                                               QGNGIQDLVKAANDLGIEVWREERSNLDIAKTSFDTTQKILGFTDRGIVLFAPQLDNLLK
                                                                                                                       MSKITLSSLKSSLQQGLKNGKNKLNQAGTTLKNGLTQTGHSLQNGAKKLILYIPQGYDSG
AGLELTNELVGNIASSVQTVDAFAEQISKLGSHLQNVKGLGGLSNKLQNLPDLGKASLGL
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                                                                                                                                                                                                                                                                                                                                                                                                              PF02382; RTX;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001343; Hemlysn_Ca_bind IPR003355; RTX_N. IPR003995; RtxA.
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47.5%;
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Pred. No. 9.46
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9.4e-107;
hes 257;
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OR CYTOLYTIC
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p55131;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
    "Genetic map of the Actinobacillus pleuropneumoniae operons: characterization of the ApxIII operons."; Infect. Immun. 62:4411-4418(1994).
                                             Jansen R., Briaire Smits M.A.;
                                                                             STRAIN=405 / SEROTYPE 8;
MEDLINE=95012630; PubMed=7927703;
                                                                                            SEQUENCE FROM N.A. STRAIN-405 / SEROJ
                                                                                                                                                                                               IIIA) (CLY-IIIA).
APXIIIA OR CLYIIIA OR RTXA OR PTXA
                                                                                                                                                                                                                               RTX-III toxin determinant A from serotype
                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                 Actinobacillus pleuropneumoniae
                                                                                                                                     NCBI_TaxID=715;
                                                                                                                                                       Actinobacillus
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Pasteurellaceae;
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                                                                Gielkens
                                    RTX-toxin
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Best Local Similarity
Matches 426; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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STRAIN-SEROTYPE 8;
MEDLINE-93162836; PubMed=8432615;
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SEQUENCE FROM N.
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Toxin; Cytolysis; Cytotoxin;
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FUNCTION: DOES NOT HAVE HEMOLYTIC ACTIVITY CONTONICITY TOWARDS ALVEOLAR MACROPHAGES A SUBCELLULAR LOCATION: Secreted.

DOMAIN: THE GLY-RICH REGION IS PROBABLY INV.
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GSSTGDAVS-KLAKSQTIISGIQSVLGTVLAGINLNEAIISGGSELE-LAEAGVSLASEL
                                     GLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEI
                                                                                                 KAADELGIARLAEEPNHTETAKKSVDTVNOFLSLTQTGIAISATKLEKFLQKHSTNKLAK 105
                                                                                                                                                          KRQAKKGYDVTKNGLQYGVSQAKLQALAAGKAVQKYGNKLVLVIPKEYDGSVGNGFFDĻV
                                                                                                                                                                                                 KSNIQAGLNSTKSGLK---
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                                                                               KAAEELGIQVKYVNRNELEVAHKSLGTADQFLGLTERGLTLFAPQLDQFLQKHSKISNVV
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PR01488;
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Pred. No. 2.2e-93;
6; Mismatches 286
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POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                          F83AFE25A6FD8758 CRC64;
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                                                                                                                                                                                   -----NLYLAIPKDYDPQKGGTLNDFI
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Calcium;
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RESULT 9
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ID RT31_A
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DT 01-OCT
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                                                      RT31_ACTPL STANDARD; PRT; 1049 AA. p55130; O1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) 30-MAY-211I toxin determinant A from serotype 2 (AD) RTX-III OR CLY-IIIA). APXIIIA OR CLYIIIA OR RTXA OR PTXA. ACTINDACIIUS pleuropneumoniae (Haemophilus pleuropneumoniae (Haemophilus pleuropneumoniae)
 Actinobacillus.
NCBI_TaxID-715;
[1]
                                            Bacteria; Proteobacteria;
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                                            gamma
                                              (Haemophilus subdivision;
                                                                                                   (APX-IIIA)
                                            pleuropneumoniae)
Pasteurellaceae;
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Matches 429
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYPOTOXICITY TOWARDS ALVEOLAR MACROHAGES AND NEUTROPHILS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYT ACTIVITY (BY SIMILARITY).
-!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
-!- PPM: PALMITOYLATED BY APXIIIC. THE TOXIN ONLY BECOMES ACTIVE WODIFIED (BY SIMILARITY).
                                                                                                                                  REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genetic map of the Actinobacillus pleuropneumoniae operons: characterization of the ApxIII operons."; Infect. Immun. 62:4411-4418(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93263992; pubMed=8494611;
Chang Y.-F., Shi J., Ma D.-P., Shin S.J.,
"Molecular analysis of the Actinobacillus
toxin-III gene cluster.";
DNA Cell Biol. 12:351-362(1993).
                                                                                                                                                                                                                                                                                               Lipoprotein; TRANSMEM
                                                                                                                                                                                                                                                                                                                       PROSITE; PS00330; HEMOLYSIN_CALCIUM; Toxin; Cytolysis; Cytotoxin; Repeat;
                                                                                                                                                                                                                                                                                                                                              Pfam; PF00353; hemolysinCabi
Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=1536 / SEROTYPE 2; MEDLINE=95012630; PubMed=7927703;
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                                                                                                                                                                                                                                                                        TRANSMEM
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KRQVKKGYDVTKNGLQYGVSQAKLQALAAGKAVQKYGNKLVLVIPKEYDGSVGNGFFDLV
                       KSNIQAGLNSTKSGLK-----
                                              al Similarity
429; Conser
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; Palmitate
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                                              Conservative
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POTENTIAL.
POTENTIAL.
11 x REPEATS,
                                             Score 1928; DB 1;
Pred. No. 9e-92;
2; Mismatches 295;
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Calcium;
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pleuropneumoniae
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HLYA_ECOLI
P08715;
01-JAN-1988
01-JAN-1988
01-MAR-2002
                                                                                                                            LLKNVTQEQNESNLSS--LKTELGKIITNAGNFGVA
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                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: BACTERIAL HEMOLYSINS
CELL MEMBRANES AND CAUSE CELL F
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                                                                                                                                                   PROSITE; PS00330; HEMOLYSIN_CALCIUM; Hemolysis; Toxin; Cytolysis; Cytotox.
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PubMed=7801126;
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nce of a plasmid-encoded hemolysin determ
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                                                 use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Bacteria; Proteobacteria;
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                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                MODIFIED.
DISEASE:
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DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN.

PMM: PALMITOYLATED BY HLYC. THE TOXIN ONLY BECOMES ACTIVE
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DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING C
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SIMILARITY:
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                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-13039 / SEROTYPE 10;
STRAIN-13039 / SEROTYPE 10;
MEDLINE-94276858; PubMed-8007819;
Magai S., Yagihashi T., Ishihama A.;
"DNA sequence analysis of an allelic pleuropneumoniae-RTX-toxin I (ApxIA)
Microb. Pathog. 15:485-495(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HLY-IA) (Cytolysin IA) (CLY-IA)
APXIA OR CLYIA OR HLYIA.
Actinobacillus pleuropneumoniae
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30-MAY-2000
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                                           Chin N., Frey J., Chang C.F., Chang "Identification of a locus involved Actinobacilus pleuropneumoniae.", FEMS Microbiol. Lett. 143:1-6(1996).
                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-K17 / SEROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
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                                                                                                                                     STRAIN=K17 / SEROTYPE 5;
MEDLINE=96401417; PubMed=8807793;
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NCBI_TaxID=715;
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                                                                                                                                                                                                                                                                                                                    PRINTS; PR00313; CABNDNGRPT PRINTS; PR01488; RTXTOXINA.
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DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: APXIA IS PARTIALLY DELETED IN SEROTYPES 8, 12, AND TOTALLY DELETED IN SEROTYPE 3.
MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF SEROTYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVITY.

DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY) PTM: PALMITOYLATED BY APXIC. THE TOXIN ONLY BECOMES ACTIVE 1
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YGEGYNALPQLRKDIEQIISSTGALTGEHGQVLVGAGGPLAYSNSPNSIPNAFSNYLTQ
                                       ADENKSO----KLSASDIASSLNKLVGS----
                                                                                                                                                                            YSKEYGRHIIIEKGGDDDTLLLSDLSFKDVGFIRIGDDLLVNKRIGGTLYYHEDYNGNAL
                                                                                                                                                                                                                                                                  NNFLNGGDGDDELQVFEGQYNVLLGGAGNDILYGSDGTNLFDGGVGNDKIYGGLGKDIYR
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                                                                                   -KIEKIVDKDGAYVLSQYLTELTAPGRGINYFNGLEEKLY
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(Rel. 34, (Rel. 34,

Last

sequence update)

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EMBL; X52899; CAA37081.1; -.
EMBL; X68595; CAA48586.1; -.
EMBL; X73117; CAA51548.1; -.
EMBL; U05042; AAB05034.1; -.
InterPro; IPR0013143; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
InterPro; IPR00395; RTXA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91348845; PubMed-1879928; Frey J., Meier R., Gygi D., Nicol "Nucleotide sequence of the hemol pleuropneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinobacillus pleuropneumoniae
Bacteria; Proteobacteria; gamma
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                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         Chang Y., Wang Y., Chin N.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ
-!- FUNCTION: ONE OF THE VIRULENCE FACTORS OF
WHICH HAS A STRONG HEMOLYTIC ACTIVITY AND
ALVEOLAR MACROPHAGES AND NEUTROPHILS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: THE GLY-RICH REGION IS PROBABLY IN
CALCIUM, WHICH IS REQUIRED FOR TARGET CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Frey J., Haldimann A., Nicolet J., Boffi "Sequence analysis and transcription of from Actinobacillus pleuropneumoniae.", Gene 142:97-102(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ISOLATE CVI 13261 / SEROTYPE 9;
MEDLINE-9336425; PubMed-8359891;
Jansen R., Briaire J., Kamp E.M., Gielkens
"Structural analysis of the Actinobacillus
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STRAIN=S 4074 / SEROTYPE
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MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TO
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MISCELLANEOUS: APXIA IS F
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DOMAIN: THE THREE
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                                      PF00353; hemolysinCabind; PF02382; RTX; 1.
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             PR00313;
PR01488;
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  PS00330; HEMOLYSIN_CALCIUM;
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HLGEKNDRIYLSSGSSIYYAGNGHDVAYYDKTDTGY--LTEDGQSAQKAGEYIVTKELKA
             KAG--NDDIFVGQGKMNIDGGDGHDRVFYSK-DGGFGNITVDGTSATEAGSYTVNRKV-A
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RESULT 14
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AC P16462
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01-AUG-1990
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30-MAY-2000
                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89359382; PubMed-2670940;
Lally E.T., Golub E.E., Kleba I.R., Taichm
Rosenbloom J.C., Gibson C.W., Demuth D.R.;
"Analysts of the Actinobacillus actinomyce
gene. Delineation of unique features and c
                          entities requires or send an email t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              toxins.";
J. Biol. Chem.
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NCBI_TaxID=714;
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leukotoxin.
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                                                                                                                                                                                                                                                 MODIFIED (BY SIMILARITY).

DISEASE: ITS TARGET CELL SPECIFICITY IS RESTRICTED TO HUMAN SOME NON-HUMAN CELLS OF THE MONOMYELOCYTIC LINEAGE.

SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                    ACTIVITY.

DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY) PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE W
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DOMAIN: THE GLY-RI
CALCIUM, WHICH IS
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FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.ACTINOMYCETEMCOMITANS MIGHT BE A CYTOTOXIN, POSSIBLY THE MEMBRANE-BOUND HEMOLYSIN.
SUBCELLULAR LOCATION: OUTER-MEMBRANE ASSOCIATED OR SECRETED (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGEGYN---ALPQLRKDIEQIISSTGAFTGDHGKVSVGSGGPL
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(Rel. 15, Last sequence up)
(Rel. 39, Last annotation
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                                6
                             a license agreement (See http://www.isb-sib.ch/announce/
to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma
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InterPro; IPR003355;
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HSSP; P04002; 1WFA.
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SGKAYVDYLKKGEELAKHSDKFTKQILDPIKGNIDLSGIKGSTT--LTFLNPLLTAGKEE
                SGKAYADAFEDGKKVEAGSN----ITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTES
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392; Conserv
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milarity 41.3%;
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; Palmitate.
POTENTIAL.
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01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-MAR-2092 (Rel. 41, Last annotation update)
Bifunctional hemolysin-adenylate cyclase precursor (Cyclolysin) (ACT)
(AC-HLY) (Contains: Calmodulin-sensitive adenylate cyclase
(EC 4.5.1.1) (ATP pyrophosphate-lyase) (Adenylyl cyclase); Hemolysin]
                                                                                                                                                                                                        Glaser P., Sakamoto H., Bellalou J. "Secretion of cyclolysin, the calmo haemolysin bifunctional protein of EMBO J. 7:3997-4004(1988).
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                                                                                   "Isolation and c
domains of Borde
Eur. J. Biochem.
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   Glaser P.,
Danchin A.;
                                   MEDLINE=89251630;
                                                                                                                                      Munier H.,
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                                                                                                                                                                                                                                                                                             STRAIN=18323;
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Bordetella pertussis adenylate
ochem, 196:469-474(1991).
                   Elmaoglou-Lazaridou
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to H., Bellalou J., Ullmann A., Danchin A.;
lolysin, the calmodulin-sensitive adenylate
                                                                                                                                    PubMed=2007407;
A.-M., Glaser P.,
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Bordetella pert
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InterPro; IPR001343; Hemlysn_Ca_t InterPro; IPR003355; RTX_N. InterPro; IPR003955; RtxA. Pfam; PF00353; hemolysinCabind; 5 Pfam; PF02380; RTX; 1. PRINTS; PR00313; CABNDNGRPT.

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PROSITE; PRINTS;

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HEMOLYSIN_CALCIUM;

EMBL;

S00893; OYBRC. S09403; S09403.

Hemlysn_Ca_bind

EMBL;

Y00545; CAA68613.1; -. X14199; CAA32411.1; -. A07292; CAA00653.1; -. A14850; CAA01202.1; -.

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MEDLINE=99214144; PubMed=10196151;

Basar T., Havlicek V., Bezouskova S., Halada P., Hackett M.,

"The conserved lysine 860 in the additional fatty-acylation

Bordetella pertussis adenylate cyclase is crucial for toxin

independently of its acylation status.";

J. Biol. Chem. 274:10777-10783(1999)

-I- FUNCTION: THIS ADENYLATE CYCLASE BELONGS TO A SPECIAL CI

BACTERIAL TOXIN. IT CAUSES WHOOPING COUGH BY ACTING ON I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MFDLINE=91266896; PubMed=2050107; Glaser P., Munier H., Gilles A.-M., Kri Sarfati R., Pellecuer C., Danchin A.; "Functional consequences of single amin calmodulin-activated adenylate cyclase EMBO J. 10:1683-1688(1991).
                                                                                                                                                                                                                                                   This
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"Phylogeny of
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SIMILARITY: IN THE N-TERMINAL S CLASS-2 FAMILY.
SIMILARITY: IN THE C-TERMINAL S PROKARYOTIC TOXIN FAMILY.
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CELL FUNCTION.
CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diph
ENZYME REGULATION: ACTIVATED BY HOST CALMODULIN.
SUBCELLULAR LOCATION: Secreted.
DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED
CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDIN
ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                      PTM: RELEASED IN A PROCESSED PTM: PALMITOYLATED BY CYAC. T
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2 (bases 1 to 2784)
Angelos,J.A., Hess,J.F. and George,L.W.
Direct Submission
Submitted (15-NOV-1999) Veterinary Medicine/Epidemiology,
Submitted (15-NOV-1999) Veterinary Medicine/Epidemiology, 11497442 2 (bases 1 (bases 1 to 2784)
Angelos,J.A., Hess,J.F. and George,L.W.
Cloning and characterization of a Moraxella bovis cytotoxin
Am. J. Vet. Res. 62 (8), 1222-1228 (2001)
21388402 Moraxella bovis. Moraxella bovis Moraxella bovis RTX toxin (mbxA) gene, complete cds Bacteria; Proteobacteria; AF205359.1 AF205359 GI:15146407 2784 gamma subdivision; Moraxellaceae; ģ DNA linear BCT 02-OCT-2001 S gene

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TGGATGCGTTTGAAGAAGGCAAACACATTAAAGCCGA 1	899 AGTCCTTAGTGGTAAAGCCTATGTG	Дb
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Potter, A., Campos, M. and Hughes, H.P.A.
Chimeric protein comprising an RTX-family
Interferon or interferon
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· · · ·	On Oct 9, 2001 this sequence version replaced gi:11762017 Location/Qualifiers e 1, .6952	COMMENT FEATURES
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Sciences,	-2001) Institute of Biomedical and Life	JOURNAL
~	Davies, R.L., Wittam, T.S. and Selander, R.K.	AUTHORS
w, Joseph land	of Infection and Immunity, University of Glasgo ding, University Avenue, Glasgow G12 800, Scot	
	-2000) Institute of Biomedical and Life	TITLE JOURNAL
	3 (bases 1 to 6952) Davies,R.L., Whittam,T.S. and Selander,R.K.	REFERENCE AUTHORS
	J. Bacteriol. 184 (1), 266-277 (2002) 11741868	JOURNAL PUBMED
	annheimia (Pasteurella) haemolytic Pasteurella trehalosi	THIE
n Operon	pbell, S. and Whittam, T.S.	AUTHORS
	1157953 157953	MEDLINE
	ica riol. 183 (4), 1394-1404	JOURNAL
xin (lktA) la)	versity and molecular evolution of the leukoto ine and ovine strains of Mannheimia (Pasteurel	TITLE
	I.S. and Selander, R.K.	REFERENCE
eae;	haemolytica. haemolytica roteobacteria; gamma subdivision; Pasteurellac	SOURCE ORGANISM
	GI:15987890	ACCESSION VERSION KEYWORDS
1-DEC-2001 sequence.	AF314503 6952 bp DNA linear BCT 21 Mannheimia haemolytica strain PH2 lktCABD operon, partial	AF314503 LOCUS DEFINITION
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FLLNLAKELQAERVIATTQQQMDNNIGDLAGISRLGEKYLSGKAYVDAREEGKHIKAD
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IDGNDGNDRLEGGKGDDILDGGNGDDFIDGGKGNDLLHGGKGDDIFVHKKGDGNUNIT
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EAYVRYEGATRIEQBKFKDFKALYKOKSLSKHELLAQENKLIEAQNELAVYRSKLNE
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GTVQOLKIHTIGGVYTTAETLMIIVEDDVLEATALVPNKDIGFVAAGQEVIIKVETF
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VESVTSINMIKAMAVAPQMTDTWDKOLASYVSSSFRVTVLATIGQQGVQLISKTVNVI
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SPTEQYQGKLSLPEIKGDISFNIFFRKSPDAPTILNIVNLEIRGGEVIGIVGRSGSG
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KLISSYSAFTSSNDSRNVLVAPTSMLDQSLSSLQFARAA"
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Davies, R.L., Campbeil, S. and Whittam, T.S. Mosaic Structure and Molecular Evolution of the Leu (1ktCABD) in Mannheimia (Pasteurella) haemolytica, glucosida, and Pasteurella trehalosi J. Bacteriol. 184 (1), 266-277 (2002)
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Direct Submission
Submitted (04-OCT-2001) Institute of Biomedical and Life Sciences,
Submitted (04-OCT-2001) Institute of Biomedical and Life Sciences,
Division of Infection and Immunity, University of Glasgow, Joseph
Black Building, University Avenue, Glasgow G12 8QQ, Scotland
Sequence update by submitter
On Oct 9, 2001 this sequence version replaced gi:11762057.

Location/Qualifiers
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Davies,R.L., Whittam,T.S. and Selander,K.A.
Direct Submission
Submitted (04-OCT-2001) Institute of Biomedical
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Direct Submission
Submitted (18-0CT-2000) Institute of Biomedical and Life Sciences,
Division of Infection and Immunity, University of Glasgow, Joseph
Black Building, University Avenue, Glasgow Gl2 8QQ, Scotland
4 (bases 1 to 658)
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Davies, R.I., Whittam, T.S. and Selander, R.K.
Sequence diversity and molecular evolution of t
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                                                                                                                                                                                           /serotype="T10"
                                                                                                                                                                                                                    /strain="PH252
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a (Pasteurella)
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                            FAYVRKYEGATRI EQEKLKDFKALYKQKSLSKHELLAQENKLI EAQNELAVYRSKLNE
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EIKTGERSVMSYLLSPLEESIT
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Sequence
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                                                                                                                                                                                                                                                                         Unclassified.
1 (bases 1 to 2794)
Potter,A.A. and Manns,J.G.
GARH-leukotoxin chimeras
Patent: US 5837268-A 5 17 NOV-1998;
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Patent: US 5969126-A 5 19-OCT-1999;
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1 (bases 1 to 2794)
Potter,A.A. and Harland,R.J.
Haemophilus somnus outer membrane pro
iron-regulated proteins
Patent: US 5985289-A 1 16-NOV-1999;
Location/Qualifiers
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                                        AAGGTGATGACAACGTATTTGTTTGGTTCTGGTACGACGGAAATTGATGGCGGTGAAGGTT
                                                  ctggcaatgacgatatctttgttggtcaaggtaaaatgaatattgatggtggagatggac
                                                                                 TAGACAATGCTGGAAATGTAACTAAAACCAAAGAAACAAAAATTATTGCCAAACTTGGTG
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VERSION KEYWORDS SOURCE REFERENCE AUTHORS TITLE RESULT 1 BD009870 LOCUS DEFINITION ACCESSION COMMENT JOURNAL ORGANISM 1 (bases 1 to 2794)

Potter, A.A. and Manns, J.G.
GnRH-leukotoxin chimeras
Patent: JP 2001502887-A 3 06
UNIVERSITY OF SASKATCHEWAN
OS Unidentified
PN JP 2001502887-A/3
PD 06-MAR-2001
PF 08-AUG-1997 JP 19985091
PF 08-AUG-1996 US 08/69
PI ANDREW A POTTER, JOHN G
PC C12N15/16, C12N15/31, C12 BD009870.1 GI:18638243 JP 2001502887-A/3. GnRH-leukotoxin chimeras BD009870 unidentified BD009870 unclassified unidentified A61K38/09, C A61K39/385 Unidentified
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QF 2001502887-A/3
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08-AUG-1997 JF 1998509192
09-AUG-1996 US 08/694865
09-AUG-1996 US 08/694865
ANDREW A POTTER, JOHN G WANNS
ANDREW A POTTER JOHN G WANNS
C12N15/16,C12N15/31,C12N15/62,C12N1/21,C07K14/285, 2794 06-MAR-2001; đq DNA linear PATC07K7/23, 31-JAN-2002

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                                      CAAAAACTGGGGCAAAAAAATTATCCTCTATATTCCCCAAAATTACCAATATGATACTG
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1 (bases 1 to 2794)

Potter,A.A., Redmond,M.J. and Hughes,H.P.A.
Enhanced immunogenicity using leukotoxin chimeras
Patent: US 5422110-A 1 06-JUN-1995;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                        Unknown.
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487 c 599 g
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Pred. No. 6.2e-133;
0; Mismatches 956;
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cgggtatagaacttgattctttaatcaaaaaaggtgatgctgcacctgatgctttggcta
                        ATGCAAATAAAGCCAAAACTGTATTATCTGGCATTCAATCTATTTTAGGCTCAGTATTGG
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123447
123447.1 GI:160
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Potter, A.A. and Harland, R.J.
Haemophilus somnus outer membrane protein iron-regulated proteins
Patent: US 5534256-A 1 09-JUL-1996;
Location/Qualifiers
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Unclassified
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38; Conservative
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Pred. No. 6.2e-133;
0; Mismatches 956;
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                                     tggaaataattactggtttgctatcaggcatttctgcaggctttgctttagcggataaaa
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1 (bases 1 to 2794)
Potter,A.A., Redmond,M.J. and Hughes,H.P.
Enhanced immunogenicity using leukotoxin
Patent: US 5708155-A 1 13-JAN-1998;
Location/Qualifiers
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Sequence 5
189774
189774.1
                                       1 (bases 1 to 2794)
Potter,A.A. and Manns,J.G.
GnRH-leukotoxin chimeras
Patent: US 5723129-A 5 03-MAR-1998;
Location/Qualifiers
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Search completed: September 15, 2002, 11:15:40 Job time: 25125 sec

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Maximum Match 100%
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SPTREMBL_19:*

Sp_acchea:*

Sp_bacteria

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Sp_human:*

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sp_organelle:*
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sp_virus:*
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sp_unclassified:*
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sp_bacteria:*
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sp_mammal:*
sp_mhc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Query Match Length I	DB	ID	Description
1		100.0		2	Q93GI2	Q93gi2 moraxella k
2		75.4		N	Q9EV24	Q9ev24 mannheimia
ω	43	75.4	953	N	Q9ETX2	Q9etx2 mannheimia
4	43	75.4	953	N	Q9ETG5	Q9etg5 pasteurella
v	43	75.4	953	N	Q9EV34	
6	43	75.4	953	N	Q9EV33	Q9ev33 pasteurella
7	43	75.4	953	N	Q9EV32	
8	43	75.4	953	N	Q9EV31	
9	43	75.4	953	N	Q9EV30	Q9ev30 pasteurella
10	43	75.4	953	2	Q9EV29	_
11	43	75.4	953	N	Q9EV27	Q9ev27 pasteurella
12	43	75.4	953	N	Q9EV26	Q9ev26 mannheimia
13	43	75.4	953	N	Q9EV25	Q9ev25 mannheimia
14	43	75.4	953	N	Q9EV23	Q9ev23 mannheimia
15	43	75.4	953	2	Q9EV28	Q9ev28 pasteurella
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44 5	43	42	41	40	39	38	37	36	S G	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
36 36	36	37	37	37	37	37	37	37	37	38	38	38	38	38	38	38	38	38	38	38	38	ω 9	42	42	43	43	43
63.2 63.2	63.2	64.9	64.9	64.9	64.9	64.9	64.9	64.9	64.9	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	68.4	73.7	73.7	75.4	75.4	75.4
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088651 marmota mon	O80380 daucus caro	Q9w4n7 drosophila	Q28298 canis famil	P97692 rattus norv	Q9qym7 cricetulus	Q9c895 arabidopsis	Q9rjk0 streptomyce	Q63779 rattus norv	6 rat	Q9p2e9 homo sapien	Q96sb2 homo sapien	ente	Q9h476 homo sapien	075300 homo sapien	018051 caenorhabdi	O25891 helicobacte	Q9v3v7 drosophila	O80148 bacteriopha	w	Q9g032 bacteriopha	Q9mbs7 staphylococ	Q90307 carassius a	013099 xenopus lae	013098 xenopus lae	Q93npl actinobacil	Q9ev22 pasteurella	Q9eud4 pasteurella

ALIGNMENTS

RESULT Q9EV24 ID Q AC Q DT 0 DT 0	Qy NA	RR	RESULT Q93G12 ID AC Q0 AC Q0 DT 0 DT 0 DT 0 CT	
JLT 2 Q9EV24 PRELIMINARY; PRT; 946 AA. Q9EV24; PRESIDENTIAL PRESIDENT	Query Match 100.0%; Score 57; DB 2; Length 927; Best Local Similarity 100.0%; Pred. No. 0.17; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 1 FLSELNKELEAE 12	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=TIFTON I; MEDLINE=21388402; PubMed=11497442; MEDLINE=21388402; PubMed=11497442; Angelos J.A., Hess J.F., George L.W.; "Cloning and characterization of a Moraxella bovis cytotoxin gene."; "Cloning and characterization of a Moraxella bovis cytotoxin gene."; Ann. J. Vet. Res. 62:1222-1228(2001). EMBL, AF205359; AAK84651.1; EMBL, AF205359; AAK84651.1; SEQUENCE 927 AA; 98845 MW; F4B703577E10A96D CRC64;	JLT 1 93G12 PRELIMINARY; PRT; 927 AA. Q3G12; Q1-DEC-2001 (TrEMBLrel. 19, Created) O1-DEC-2001 (TrEMBLrel. 19, Last sequence update) O1-DEC-2001 (TrEMBLrel. 19, Last annotation update) RTX TOXIN. RBXA. MBXA. MBXA. MOTAXElla bovis. Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella. NCBI_TaxID-476;	

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Matches
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Best Local :
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Davies R.L., Whittam T.S., Selander R.K.;

"Sequence diversity and molecular evolution of the gene in bovine and ovine strains of Mannheimia (Pa haemolytica.";

J. Bacteriol. 0:0-0(2001).

EMBL; AF314518; AAG40302.1; -.

EMBL; AF314517; AAG40301.1; -.

EMBL; AF314517; AAG40301.1; -.

InterPro; IPR001753; Enoyl_CoA_hydrtse.

InterPro; IPR001343; Hemlysn_Ca_bind.

InterPro; IPR003355; RTX_N.

Pfam; PF00353; hemolysinCabind; 1.

Pfam; PF00382; RTX; 1.
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Q9ETX2;
01-MAR-2001
01-MAR-2001
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PROSITE;
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Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRAT
SEQUENCE 946 AA; 101480 MW; 25
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MEDLINE-21101823; PubMed-11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of
"Sequence Diversity and Molecular Evolution of
                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF314521; AAG40305.1; InterPro; IPR001343; Hemlysn_Ca_bind. InterPro; IPR001343; Hemlysn_Ca_bind. InterPro; IPR003355; RTX_N.
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Bacteria; Proteobacteria;
Mannheimia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=85401;
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); PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
)E 953 AA; 102135 MW; 70DB354157F5881E
                                                                         Similarity 75. 9; Conservative
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                                                                       Score 43; DB Pred. No. 45; 1; Mismatches
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Last sequence update)
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MW; 25C077858BDC76C4
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                                                                                                               Length 953
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STRAIN=H1284, PH388, AND PH8;
STRAIN=H284, PH388, AND PH8;
STRAIN=H284, PH388 T.S., Selander R.K.;
Davies R.L., Whittem T.S., Selander R.K.;
"Sequence diversity and molecular evolution of the
"Sequence diversity and molecular evolution of the
gene in bovine and ovine strains of Mannheimia (Pa
haemolytica.";
J. Bacteriol. 0:0-0(2001).
EMBL; AF314507; AAG40291.1; -.
EMBL; AF314506; AAG40298.1; -.
EMBL; AF314506; AAG40288.1; -.
EMBL; AAG40288.1; -.

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Q9EV34;
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SEQUENCE
J. Bacteriol. 183:1394-1404(2001).
EMBL; AF314505; AAG40789.1; -.
InterPro; IPR001753; Encyl_CoA_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
                                                                                                                                                                                       MEDLINE-21101823; PubMed-11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of
Gene in Bovine and Ovine Strains of Mannheimia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pasteurella
Bacteria; Pı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00353; hemolysinCabind; Pfam; PF02382; RTX; 1. PRINTS; PR00313; CABNDNGRPT.
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Mannheimia
                                                                                                                                                                haemolytica.";
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mannheimia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKTA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pasteurella haemolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9ETG5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEUKOTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 75.4%;
Similarity 75.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
953 AA; 101997 MW; D593D6A577C3ADE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteobacteria;
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                       the Leukotoxin
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(Pasteurella)
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Matches 9
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                                                                                                                                                                                                                                                              haemolytica.";

J. Bacteriol. 183:1394-1404(2001).

EMBL; AF314508; AAG40292.1;

InterPro; IPR001753; Enoyl_CoA_hydrt.
InterPro; IPR001343; Hemlysn_Ca_bind
InterPro; IPR003355; RTX_N.

Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF00353; CABUNGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATAS
SEQUENCE 953 AA; 102132 MW; 4138.
                                                                            Q9EV32
Q9EV32;
Q1-MAR-2001
Q1-MAR-2001
Q1-DEC-2001
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01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 953 AA; 102010 MW; DE48B28EE0EB09FB CRC64;
                                                          LKTA.
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21101823; PubMed-11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of the Leukotoxin
Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
                                      Pasteurella haemolytica.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9EV33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9EV33
                                                                     LEUKOTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pasteurella haemolytica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001
SEQUENCE FROM N.A.
                   NCBI_TaxID=75985;
                             Mannheimia
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=75985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mannheimia
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                                                                                                                                                                         FLLNLNKELOAE
                                                                                                                                                                                                              h 75.4%;
Similarity 75.0%;
9; Conservative
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1 (TrEMBLrel. 16,
1 (TrEMBLrel. 19,
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                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                 ENOYL_COA_HYDRATASE; UNKNOWN_1.
; 102132 MW; 4138AB5FAE2843B3
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75.0%;
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Hemlysn_Ca_bind.
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                                      gamma
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Last sequence update)
Last annotation updat
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Last sequence update)
Last annotation updat
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                                                                                                                       PRT;
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                                      subdivision;
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RESULT Q9EV30

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Q9EV30;

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Q9EV31;
01-MAR-2001
01-MAR-2001
01-DEC-2001
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EMBL; AF314509; AAG40293.1; -
InterPro; IPR001753; Emoyl_CoA_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX.N.
Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF00383; RTX; 1.
PRINTS; PR00313; CABNDMGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
EROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
                                                                                                                               Pfam; PF00353; hemolysinCabind; 1. Pfam; PF02382; RTX; 1. PRINTS; PR00313; CABNDNGRPT.
                                                                                                                                                                     J. Bacteriol. 183:1394-1404(2001).
EMBL; AF314510; AAG40294.1; ...
InterPro; IPR001753; Enoyl_Coa_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
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"Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA)
Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
haemolytica.";
                                                                                                                                                                                                                                MEDLINE=21101823; PubMed=11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution
Gene in Bovine and Ovine Strains of Mannhein
haemolytica.";
                                                                                                           PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 953 AA; 102160 MW; A189BF80754A7907
                                                                                                                                                                                                                                                                                                                                                          Pasteurella haemolytica.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                               STRAIN-PH588;
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    LKTA
                                                                                                                                                                                                                                                                                                                                                                                                LEUKOTOXIN.
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451
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                     1 FLSELNKELEAE
FLUNENKELQAE
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                                              Similarity
9; Conserv
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9; Conserv
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(TrEMBLrel. 16,
(TrEMBLrel. 19,
                                               Conservative
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462
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                                              Score 43; DB
Pred. No. 45;
1; Mismatches
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Pred. No. 45;
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Best Local
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                                        J. Bacteriol. 183:1394-1404(2001).

EMBL: AF314514; AAG40298.1; -
InterPro; IPR001753; Enoyl_Coa_hydrt
InterPro; IPR001343; Hemlysn_Ca_bind
InterPro; IPR003355; RTX_N.

Pfam: PF00353; hemolysinCabind; 1.
Pfam: PF00353; RTX; 1.
PRIMTS; PR00313; CABNUGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATAS
SEQUENCE 953 AA; 102147 MW; 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 183:1394-1404(2001).

EMBL; AF314512; AAG40296.1;

Interpro; IPR001753; Enoyl_Coa_hydrtse.
Interpro; IPR001343; Hemlysn_Ca_bind.
Interpro; IPR003355; RTX_N.

Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF02382; RTX; 1.
Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABUNDGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UN
SEQUENCE 953 AA; 102043 MW; 4E8F11490
                                                                                                                                                                                                                                                                                                Q9EV29
Q9EV29;
Q1-MAR-2001
Q1-MAR-2001
Q1-DEC-2001
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01-MAR-2001
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                                                                                                                                                                         STRAIN=PH278;
MEDLINE=21101823; PubMed=11157953;
Davies R.L., Whittam T.S., Selande
                                                                                                                                                               Gene
                                                                                                                                                                                                                                                                              LKTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; F
Mannheimia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pasteurella haemoıyı....
Pacteria; Proteobacteria;
                                                                                                                                                "Sequence Diversity and Megene in Bovine and Ovine haemolytica.";
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       Pasteurella haemolytica.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                        LEUKOTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Davies R.L., Whittam T.S., Selande "Sequence Diversity and Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKTA
                                                                                                                                                                                                                                    NCBI_TaxID=75985;
                                                                                                                                                                                                                                                Mannheimia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haemolytica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21101823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=PH196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=75985;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                              451
   Local
                                                                                                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                                                                                                             FLLNLNKELQAE
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  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine and Ovine
                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
9; Conser
                                                                                                                                                                                                                                                                                                (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                     75.4 ilarity 75.0 Conservative
                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                          ENOYL_COA_HYDRATASE;
; 102147 MW; 11600FI
                                                                                                                                                                                                                                                                                                                                                                                              462
                                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=11157953;
                                                                                                     Enoyl_CoA_hydrtse.
Hemlysn_Ca_bind.
  75.
75
                                                                                                                                                                                                                                                                                                                                                                                                                                                . 08;
   . 4%;
                                                                                                                                                                      Molecular
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16,
19,
                                                                                                                                                          Molecular Evolution of Strains of Mannheimia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ., Selander R.K.; Molecular Evolution of Strains of Mannheimia
                                                                                                                                                                                                                                                       gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma
                                                                                                                                                                               Selander R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB Pred. No. 45; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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  Score
Pred.
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                                          RATASE; UNKNOWN_1
11600FDA7849A1CA
                                                                                                                                                                                                                                                       subdivision;
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                                                                                                                                                                                                                                                                                                 sequence update) annotation updat
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 43;
No.
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DB · 45;
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                                                                                                                                                                                                                                                       Pasteurellaceae;
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         Length 953
                                                                                                                                                           (Pasteurella)
                                                                                                                                                                     the Leukotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the Leukotoxin (Pasteurella)
                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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OPEV26

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Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9EV26;
01-MAR-2001
01-MAR-2001
01-DEC-2001
LEUKOTOXIN.
MEDLINE-21101823; PubMed-11157953;
Davies R.L., Whittam T.S., Selander R.K.;
Sevenence Diversity and Molecular Evolution of Gene in Bovine and Ovine Strains of Mannheimia haemolytica.";
J. Bacteriol. 183:1394-1404(2001).
EMBL; AF314519; AAG40303.1; -.
InterPro; IPR001753; Enoyl_CoA_hydrtse.
                                                                                                                                                                                                                                                                                                                                                                            Mannheimia glucosida
Bacteria; Proteobacto
Mannheimia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 183:1394-1404(2001).

EMBL; AF314516; AAG40300.1; -.

InterPro; IPR0011753; Encyl_CoA_hydrtse.

InterPro; IPR001343; Hemlysn_Ca_bind.

InterPro; IPR003355; RTX_N.

Pfam; PF00353; hemolysinCabind; 1.

Pfam; PF02382; RTX; 1.
                                                                                                                                                                                                                                                         STRAIN-PH240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21101823; PubMed=11157953; Davies R.L., Whittam T.S., Selande
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Mannheimia.
NCBI_TaxID=75985;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=85401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence Diversity and Molecular Gene in Bovine and Ovine Strains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKTA
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pasteurella haemolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00313; CABNDNGRPT.
; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
E 953 AA; 102230 MW; 2B686808EB370090
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9; Conser
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16,
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19,
                                                                                                                                                                                                                                                                                                                                                                                                               gamma
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lecular Evolution of
trains of Mannheimia
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                            subdivision; Pasteurellaceae;
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annotation update)
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45;
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                                                                                                                               (Pasteurella)
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(Pasteurella)
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JR InterPro; IPR003355; RTX_N.

DR Pfam; PF00353; hemolysinCabind; 1.

DR Pfam; PF02382; RTX; 1.

DR PRINTS; PR003115; ENOYL_COA_HYDRATASE; UNKNOWN_1.

DR PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.

PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.

PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.

DR PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.

DR PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.

PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
RESULT
Q9EV23
ID Q9
AC Q9
AC Q9
AC Q9
DT 01
DT 0
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Best Local
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Best Local :
                                                                                                                                                                                       Q9EV23;
Q9EV23;
Q1-MAR-2001;
Q1-MAR-2001;
Q1-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9EV25;
01-MAR-2001
01-MAR-2001
01-DEC-2001
                        Mannheimia glucosida.
Bacteria; Proteobacteria;
Mannheimia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF314520; AAG40304.1;
InterPro; IPR001753; Enoyl_CoA_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21101823; PubMed=11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution
Gene in Bovine and Ovine Strains of Mannheim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0313; CABNDNGRPT.

PROSITE; PSO0166; ENOYL_COA_HYDRATASE; UNKNOWN_1.

SEQUENCE 953 AA; 102138 MW; C41D9EBC1D799951 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mannheimia glucosida.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9EV25
                                                                                                                                                                  LEUKOTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 183:1394-1404(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEUKOTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haemolytica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=85401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mannheimia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLLNLNKELQAE 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLLNLNKELQAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00353; hemolysinCabind; PF02382; RTX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
9; Conserv
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9; Conserv
                                                                                                                                                                                              (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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75.0%;
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16,
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                                                              gamma
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Last annotation update)
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                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB Pred. No. 45; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                              subdivision;
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Mannheimia
                                                                                                                                                                                                                                                                                                                                     953
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45;
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45;
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                                                                 Pasteurellaceae;
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(Pasteurella)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leukotoxin (lktA)
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Best Local
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Q9EV28;
01-MAR-2001
01-MAR-2001
01-DEC-2001
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SEQUENCE FROM STRAIN-PH290;
                                                                                                   "Mosaic structure and molecular evolution of the leukotoxin of (lktCABD) of Mannheimia (pasteurella) haemolytica, Mannheimia jucosida and Pasteurella trehalosi.";

J. Bacteriol. 0:0-(0:2001).

EMBL; AF314515; AAG40299.1; -.

EMBL; AF314515; AAG40299.1; -.

EMBL; AF314141; AAL13281.1; -.

InterPro; IPR001753; Enoyl_CoA_hydrtse.

InterPro; IPR001343; Hemlysn_Ca_bind.

InterPro; IPR003355; RTX_N.

PEam; PP00353; hemolysinCabind; 1.
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InterPro; IPR001753; Encyl_CoA_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR001345; RTX_N.
Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF00353; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 953 AA; 102150 MW; D99C36DA595B1624 (
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Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 953 AA; 102218 MW; 04AB1715B819E571 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRALN-PH292, AND PH296;
MEDLINE-21101823; Pubwed-11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evoluti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pasteurella haemolytica.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-PH296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEUKOTOXIN (LKTA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      Davies R.L., Campbell
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        haemolytica."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=75985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mannheimia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   haemolytica."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FLSELNKELEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in Bovine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183:1394-1404(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                      S., Whittam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular Evolution of Strains of Mannheimia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D99C36DA595B1624 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      T.S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Pasteurella)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the Leukotoxin (1ktA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
```

Query Match Best Local Similarity

75

. 4.8

Score Pred.

No.

DB 45;

2

Length 953;

. 0	Search completed: September 11, 2002, 09:01:26 Job time: 284 sec	Oy 1 FLSELNKELEAE 12 Db 451 FLLNLNKELQAE 462	Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps
			0;

RESULT 1 AAF57290 ID AAF57290 standard; DNA; 3231 BP

AAF57290;

Moraxella; antigen; immune response; infection; RTX toxin; vaccine; antibacterial; ds. 29-MAY-2001 (first entry) CDS M. bovis Dalton 2d RTX toxin A subunit encoding DNA. CDS Moraxella bovis. CDS Location/Qualifiers 232..3015 /*tag= b 'note= "partial coding region of RTX toxin C subunit" 1080..3250 /*tag= c /note= "partial coding region of RTX toxin B subunit" '*tag= a
'product= "RTX toxin A subunit"

31-AUG-2000; 2000WO-AU01048.

WO200116172-A1.

08-MAR-2001.

```
RESULT
AAB62110
                                                                                                                                                          SX X C C C C C C C X X S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB62110 standard; Protein; 927 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moraxella; antigen; immune response; infection; RTX toxin; vaccine; antibacterial; A subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB62110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M. bovis Dalton 2d RTX toxin A subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200116172-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moraxella bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-AUG-2000; 2000WO-AU01048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-AUG-1999;
                                                                 100.0%; Score 77; DB 22; Length 927; Query Match 100.0%; Pred. No. 7.4e-05; Best Local Similarity 100.0%; Pred. No. 7.4e-0; Indels 0 Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Farn J, Strugnell R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CSIR ) COMMONWEALTH SCI & IND RES ORG. (UYME ) UNIV MELBOURNE.
                                                                                                                                                                                                                                                                                                                                                                                            Novel Moraxella bovis antigen useful in compositions for raising immune response in an animal, has protease, lipase or hemolysin activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAF57290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-235092/24.
                                                                                                                                                                                           The invention relates to new Moraxella bovis antigens and nucleic acid sequences encoding these antigenic polypeptides. The antigenic sequences encoding these antigenic sequences encoding these antigenic response in an animal directed against Moraxella, preferably against response in an animal directed against Moraxella infections. The M. bovis or M. catarrhalls, and for treating Moraxella infections. The present sequence represents the amino acid sequence of the A subunit of the RTX toxin from M. bovis Dalton 2d.
                                                                                                                                                                                                                                                                                                                                              Claim 26; Fig 5; 60pp; English.
                                                                                                                                                              Sequence
1 FNDIFHSGEGDDLL 14
|||||||||||||||
| 705 fndifhsgegddll 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99AU-0002571.
                                                                                                                                                                          927 AA;
                                                                                                                0; Gaps
                                                                                                                          .
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ALIGNMENTS

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SEQ 6
RESULT
ID
     AAB62110 standard; Protein; 927 AA.
хx
     AAB62110;
XX
DT
     29-MAY-2001 (first entry)
XX
     M. bovis Dalton 2d RTX toxin A subunit.
ХX
     Moraxella; antigen; immune response; infection; RTX toxin;
KW
XX
     antibacterial; A subunit.
     Moraxella bovis.
XX
PN
     WO200116172-A1.
XX
PD
XX
PF
     08-MAR-2001.
     31-AUG-2000; 2000WO-AU01048.
XX
PR
     31-AUG-1999;
                   99AU-0002571.
ХΧ
     (CSIR ) COMMONWEALTH SCI & IND RES ORG.
PA
     (UYME ) UNIV MELBOURNE.
ΧX
ΡI
     Farn J, Strugnell R, Tennent J;
ХΧ
DR
     WPI; 2001-235092/24.
     N-PSDB; AAF57290.
XX
     Novel Moraxella bovis antigen useful in compositions for raising immune
PТ
     response in an animal, has protease, lipase or hemolysin activity
```

```
PS Claim 26; Fig 5; 60pp; English.

XX

The invention relates to new Moraxella bovis antigens and nucleic acid sequences encoding these antigenic polypeptides. The antigenic polypeptides and polynucleotides are useful for raising an immune response in an animal directed against Moraxella, preferably against M. bovis or M. catarrhalis, and for treating Moraxella infections. The present sequence represents the amino acid sequence of the A subunit of the RTX toxin from M. bovis Dalton 2d.

Sequence 927 AA:
```

```
Query Match 100.0%; Score 57; DB 22; Length 927; Best Local Similarity 100.0%; Pred. No. 0.2; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

·88 ·

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RESULT
AAR86998
          AAR86998 standard; Protein; 758 AA.
ХX
          AAR86998;
          04-JUL-1996 (first entry)
DT
XX
          Enterohaemorrhagic E.coli hlyA gene product.
         Enterohaemorrhagic Escherichia coli; virulent; EHEC; O157:H7 serotype; detection; probe; primer; hlyA gene; enterohaemorrhagic colitis; haemolytic uremic syndrome; mesenteric adenitis.
ХX
ΚW
KW
KW
XX
          Escherichia coli (enterohaemorrhagic).
os
          US5475098-A.
PN
 ХX
          12-DEC-1995.
XX
PF
                                        94US-0258188.
          14-JUN-1994;
          14-JUN-1994;
                                         94US-0258188.
 PR
 XX
           (USSH ) US DEPT HEALTH & HUMAN SERVICES.
 ХX
           Hall RH, Xu JG;
 XX
DR
          WPI; 1996-048546/05.
N-PSDB; AAT08098.
 DR
           Entero:haemorrhagic E. coli (EHEC) nucleic acid sequences - useful for probe and primer design for sensitive and specific detection of EHEC
 XX
PT
 PT
XX
PS
XX
CC
CC
CC
CC
CC
CC
CC
           Claim 1; Columns 37-42; 32pp; English.
          Enterohaemorrhagic E.coli (EHEC) associated with enterohaemorrhagic colitis, haemolytic uremic syndrome and mesenteric adenitis have been found to carry a hlyA gene and a hylB gene, separated by an intergenic region. The hly genes and the intergenic region are absent from bacteria not associated with these diseases and so provide a useful target for detecting EHEC pathogens, esp. 0157:H7 serotype E.coli. The present sequence is that of the protein encoded by the EHEC hlyA gene.
            Sequence 758 AA;
      Query Match 67.5%; Score 52; DB 17; Length 758; Best Local Similarity 57.1%; Pred. No. 1.4; Matches 8; Conservative 3; Mismatches 3; Indels
                                                                                                                                     0; Gaps
                  1 FNDIFHSGEGDDLL 14
  Qу
              |||||| :|:| :
480 fndifhgadgndyi 493
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RESULT
AAW22159
           AAW22159 standard; Protein; 1049 AA.
ID
ХX
            16-FEB-1998 (first entry)
DT
DE
            ApxIIIB protein.
ХX
            RTX toxin; apxICA gene; apxIBD gene; apxIIAB'C gene; apxIIIABCD gene; repeat in toxins toxin; cell-associated RTX toxin; vaccine production; therapy; A. pleuropneumoniae infection; swine pleuropneumonia.
KW
            Actinobacillus pleuropneumoniae.
os
ХX
            CA2170839-A.
XX
PD
            02-SEP-1996.
                                                 96CA-2170839.
PF
            01-MAR-1996:
ХX
            01-MAR-1995;
                                                 95US-0396244.
XX
PA
             (UYGU-) UNIV GUELPH.
            MacInnes J, Mallard B, Ricciatti P, Rosendal S;
PΙ
            WPI: 1997-245536/23
DR
            N-PSDB; AAT73220.
DR
            Preparations of microorganisms producing cell-associated RTX toxins - especially for production of vaccines against swine \,
PT
XX
             pleuro-pneumonia
             Disclosure; Pages 107-110; 151pp; English.
CC
           AAW22151-W22161 represent A. pleuropneumoniae RTX (repeat in toxins) toxins. These sequence are encoded by the apxICA, apxIBD, apxIIABCC, and apxIIIABCD genes (see AAT73217-T73220), and can be expressed by microorganisms used in the preparations of the invention. The preparations are bacterial preparations comprising one or more isolated and purified strains of a microorganism that produces one or more RTX toxins, where the strains have at least one cell-associated RTX toxin. The preparations are used for production of vaccines for the prophylaxis and treatment of infectious diseases caused by microorganisms that produce RTX toxins, where the strains have been attenuated or inactivated. The vaccines are preferably against Actinobacillus pleuropneumoniae infection (swine pleuropneumonia). It has been found that A. pleuropneumonia produces significant quantities of cell-associated RTX toxins when cultured under certain conditions, and
             AAW22151-W22161 represent A. pleuropneumoniae RTX (repeat in toxins)
            that the whole-cell protein composition of the cultures corresponds to the whole-cell protein profiles obtained from cells recovered at necropsy from the pleural fluid of infected swine. Vaccination with a bacterin prepared from heat-inactivated cultures having significant quantities of cell-associated RTX toxins give significant protection of swine against challenge with homologous strains.
CC
 CC
             swine against challenge with homologous strains.
              Sequence 1049 AA;
                                                                  75.3%; Score 58; DB 18; Length 1049;
71.4%; Pred. No. 0.18;
tive 1; Mismatches 3; Indels
       Query Match
                                                                                                                                                                    0; Gaps
        Best Local Similarity
                               10: Conservative
                       1 FNDIFHSGEGDDLL 14
   Qy
                  747 frdifhgadgddll 760
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2992 ggaattttggctccaagtgtttag 3015

2540

aatattgatggtggagatggacacgatcgtgtcttctatagtaaagacggaggatttggt 1860 032 aatattgatggtggagatggacacgatcgtgtcttctatagtaaagacggaggatttggt 2091 tctaccgataatttgaaatcagtagaagaagtaattggttctcaatttaatgatgtattc 2100 tctaccgataatttgaaatcagtagaagaagtaattggttctcaatttaatgatgtattc 2331 :272 aaaggttctaaattcaacgacatattccatagtggtgaaggtgatgatttactcgatggt 2160 all the state of t ggcgatgatttactcgatggcggttctggtgatgatgtattaaatggtggtgctggtaat 2280 ggcgatgatttactcgatggcggttctggtgatgatgtattaaatggtggtgctggtaat 2511 2341 gataaattagcatttgcagatgcaaatatatctgatattatgattgaacgtaccaaagag 2400 gataaattagcatttgcagatgcaaatatatctgatattatgattgaacgtaccaaagag 2631 2572 ggtattatagttaaacgaaatgatcattcaggtagtattaacataccaagatggtacata 2460 វីវិស៊ីស៊ីស៊ីអ៊ីអាស៊ីអាស៊ីអាអាអាស៊ីស៊ីវិស្សាយប្រជាធារីប្រើប្រាជា ggtattatagttaaacgaaatgatcattcaggtagtattaacataccaagatggtacata 2691 ggtaaagatggtagttatatcacttccgatcaaattgataaaattttgcaagataagaaa 2580 2752 ggtaaagatggtagttatatcacttccgatcaaattgataaaattttgcaagataagaaa 2811 2812 aaattatetgetteggacattgcaagtagettaaataagetagttgggteaatggcacta 2700 2872 aaattatctgcttcggacattgcaagtagcttaaataagctagttgggtcaatggcacta 2931 ggaattttggctccaagtgtttag 2784 iimmiimmiimmii

741 ggtctaatagtaaatgcaaaagctggcaatgacgatatctttgttggtcaaggtaaaatg 1800 ggtctaatagtaaatgcaaaagctggcaatgacgatatctttgttggtcaaggtaaaatg 2031

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RESULT
AAQ10727
   · AAQ10727 standard; DNA; 2788 BP.
XX
      AAQ10727;
AC
      11-APR-1991 (first entry)
DT
      Leukotoxin 352 gene in plasmid pAA352
XX
       LKT; vaccine; antigen; respiratory disease; shipping fever pneumonia;
X X
KW
       Pasteurella haemolytica Al strain B122.
ХX
OS
 ХX
       CA2014033-A.
 PN
 ХX
        07-OCT-1990.
 PD
                            90CA-2014033.
        06-APR-1990;
 PF
 XX
                             89US-0335018.
        07-APR-1989;
 XX
        (UYSA-) UNIV SASKATCHEWAN.
        Acres SD, Babiuk LA, Potter AA, Lawman MJP;
 XX
PI
        WPI; 1991-000097/01.
  DR
         P-PSDB; AAR10889
         Pasteurella haemolytica proteins and genes - used for producing vaccines to protect animals esp. cattle from respiratory diseases
  DR
  PT
         e.g. pneumonia.
  PT
XX
PS
         Claim 13; Fig 5; 87pp; English.
         Plasmid pAA352 is derived from pAA114, a clone isolated from a genomic library of P. haemolytica. The protein encoded by the plasmid, "new leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin. LKT 352 and pref. antigenic fragments of it, authentic leukotoxin. LKT 352 and pref. artigenic fragments of it, authentic leukotoxin. LKT 352 and pref. artigenic fragments of it, authentic leukotoxin. LKT 352 and pref. artigenic fragments of it, authentic leukotoxin. They can also be used to produce antibodies for immunoaffinity They can also be used to produce antibodies for immunoaffinity purificn. of further proteins. [Fig. contg. sequence v. poor] See also AAR10890, AAR20909, AAR10910 and AAQ10783.
   CC
   CC
CC
   CC
   CC
          Sequence 2788 BP; 928 A; 487 C; 597 G; 776 T; 0 other;
      Query Match 29.4%; Score 817.6; DB 12; Length 2788; Best Local Similarity 60.0%; Pred. No. 3.5e-171; Matches 1530; Conservative 0; Mismatches 964; Indels 54;
                                                                                            54; Gaps
              Qy
             DЪ
    Ov
             Db
     Qy
             Dр
     Qy
              Dр
      Qy
      Db
              353 gtaaagcaagtaatgtattatcaacattaagctcttttttgggcactgcattagcgggta 412
```

```
SEQ10
RESULT
AAR10889
        AAR10889 standard; Protein; 924 AA.
ID
XX
        AAR10889;
XX
DT
        11-APR-1991 (first entry)
XX
DE
        Leukotoxin 352 encoded by plasmid pAA352.
        LKT; vaccine; antigen; respiratory disease; shipping fever pneumonia.
KW
XX
         Pasteurella haemolytica Al strain B122.
XX
PN
         CA2014033-A.
         07-OCT-1990.
PD
         Q6-APR-1990;
                                   90CA-2014033.
             -APR-1989;
                                   89US-0335018.
           UYSA-) UNIV SASKATCHEWAN.
          cres SD, Babiuk LA, Potter AA, Lawman MJP;
         WPI; 1991-000097/01.
         N-PSDB; AAQ10272.
DR
        Pasteurella haemolytica proteins and genes - used for producing vaccines to protect animals esp. cattle from respiratory diseases
PT
PT
         e.g. pneumonia.
XX
PS
         Claim 13; Fig 5; 87pp; English.
XX
CC
CC
        Plasmid pAA352 is derived from pAA114, a clone isolated from a genomic library of P. haemolytica. The protein, designated "new leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin. LKT 352 and pref. antigenic fragments of it, can be used in vaccines to protect cattle from respiratory diseases. They can, also be used to produce antibodies for immunoaffinity purifich. of further proteins. [Fig. contg. sequence v. poor]. See also AAR10890, AAR10909, AAR10910 and AAQ10783.
CC
CC
CC
         Sequence 924 AA;
        Query Match 63.6%; Score 49; DB 12; Length 924; Best Local Similarity 58.3%; Pred. No. 5.7; Matches 7; Conservative 3; Mismatches 2; Indels
                    2 NDIFHSGEGDDL 13
      Qy
                ||: | |:|||:
745 ndllhggkgddi 756
```

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RESULT
    leukotoxin A - Pasteurella haemolytica (serotype 1)
    C;Species: Pasteurella haemolytica (serotype 1)
C;Species: Pasteurella haemolytica
C;Date: 12-Oct-1989 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
C;Accession: B30169; C32051; S29516
    R;Highlander, S.K.; Chidambaram, M.; Engler, M.J.; Weinstock, G.M. DNA 8, 15-28, 1989
    A;Title: DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster.
   A; Reference number: A30169; MUID:89210283
A; Accession: B30169
    A; Status: not compared with conceptual translation
   A; Status: not compared with conceptual translation
A; Molecule type: DNA_
A; Residues: 1-953 <HIĞ>
R; Strathdee, C.A.; Lo, R.Y.C.
J. Bacteriol. 171, 916-928, 1989
A; Title: Cloning, nucleotide sequence, and characterization of genes encoding the
A; Reference number: A32051; MUID:89123172
A: Accession: C32051
   A; Accession: C32051
   A; Status: not compared with conceptual translation
   A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 947-953 <STR>
R; Lo, R.Y.C.; Strathdee, C.A.; Shewen, P.E.
Infect. Immun. 55, 1987-1996, 1987
   A:Title: Nucleotide sequence of the leukotoxin genes of Pasteurella haemolytica Al
   A; Reference number: S29515; MUID:87306837
   A; Accession: S29516
   A;Molecule type: DNA
A;Residues: 1-741,'D',743-953 <LOR>
A;Cross-references: EMBL:M20730; NID:g150492; PIDN:AAA25529.1; PID:g150494
   C; Comment: This organism causes bovine pneumonic pasteurellosis (shipping fever).
   C; Genetics:
   C; Function:
  C;Function:
A;Description: lyses leukocytes
C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem 1
F;238-784/Domain: hemolysin A homology <HLYA>
F;716-807/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F;554/Binding site: palmitate (Lys) (covalent) #status predicted
     Query Match 50.0%; Score 2325; DB 1; Length 953; Best Local Similarity 49.9%; Pred. No. 1.6e-111; Matches 464; Conservative 175; Mismatches 264; Indels 2
                                                                                                               26;
  Qy
                8 KSNIQAGLNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTET 65
              Db
              66 AKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLS 125
  Qy
             Db
  Qy
           Db
           Qν
 Db
 Qy
            245 GFELSNOVIGNVTKAISSYVLAORVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFN 304
           Db
           Qy
 Db
          Qy
 Db
 Qy
           425 AYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDG 484
          | | | :|:|| | ||||:||||||||:||||:|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
 Db
          Qy
Db
Qy
          545 FGRVKNWQVTDGEASSKLDFSKVIQRV------AETEGTDEIGLIVNAKAGNDDIFVGQ 597
          Db
Qy
                GKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETK 657
          Db
          658 VGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDL 717
Qy
          Db
Οv
          718 LDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDG 777
          Db
Qy
          778 TGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTD 833
          Db
Qу
          834 HKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNK 893
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